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PATENT  
0147-0211P

IN THE U.S. PATENT AND TRADEMARK OFFICE

APPLICANT: Rosenthal, Andre et al. CONF: 7286  
SERIAL NO.: 09/647,377 GROUP: 1632  
FILED: September 27, 2000 EXAMINER: PRIEBE, S.  
FOR: NUCLEIC ACID MOLECULES ENCODING PROTEINS  
WHICH INFLUENCE BONE DEVELOPMENT

## DECLARATION SUBMITTED UNDER 37 C.F.R. § 1.132

Honorable Commissioner  
Of Patents and Trademarks  
Washington, D.C. 20231

February 26, 2003

Sir:

I, Andreas Rump of the metaGen Pharmaceuticals GmbH, Germany, do hereby  
declare the following:

I have attached a copy of my curriculum vitae to this Declaration.

I am Research Scientist, of the Oncology Department and have conducted the  
experiments described below.

I am an co-inventor of the above referenced patent application and am familiar  
with the development, usages and properties of LOBO ("long-bone") proteins described  
therein.

I have read and understand the subject matter of the Office Action of September  
3, 2002.

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The following comments are offered in support of the patentability of the instant invention.

I have performed two types of searches to demonstrate the similarity between the murine LOBO protein and the human homolog LOBO protein described in the instant invention. In the first search, I used LALIGN to compare both the protein and the DNA sequences of the murine and human LOBO sequences. This search was done using the complete sequence of the murine LOBO protein/DNA disclosed in the application and the partial sequence of the human as known at the time of filing as well as the complete sequence as determined after the filing date of the instant application. LALIGN compares two protein or DNA sequences for local similarity and shows the local sequence alignments. LALIGN uses code developed by X. Huang and W. Miller (Adv. Appl. Math. (1991) 12:337-357) for the "sim" program. LALIGN will report a specified number of alignments (the default is 10) between the two sequences and their scores. The results of these comparisons are attached hereto as Appendices I (comparison of the complete mouse sequences v. partial human sequences known at the time of filing) and II (comparison of the complete mouse sequences v. complete human sequences as determined after the application was filed).

The results in Appendix I indicate that the sequence identity between the LOBO Coding Sequences of the Mouse (complete) v. Man (partial) was 85.2%. The sequence identity between the Mouse (complete) v. Man (partial) in the LOBO Protein-Alignment was 88.1% and the protein sequence similarity was 94.8%. The results in Appendix II indicate that the sequence identity for the LOBO Coding Sequences of the Mouse (complete) and Man (complete) was 85.9%. The sequence identity between the Mouse (complete) and Man (complete) in the LOBO Protein-Alignment was 88.3% and the protein sequence similarity was 96.2%. The results in Appendix II which compares the Mouse (complete) to Man (complete) further demonstrates the high degree of conservation between the murine and human DNA and protein sequences.

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I also performed a BLAST search (See, Altschul, S. et al. (1997) "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", *Nucleic Acids Res.* 25:3389-3402) to locate similar sequences using as query the complete mouse LOBO protein sequence shown as SEQ ID No: 9 in the present application (see Annex 1; 870 amino acid residues). The blast search was done via the NCBI website (<http://www.ncbi.nlm.nih.gov/BLAST/>) against the complete translated GenBank database on January 29, 2003 (blastP). The complete results are summarized in Table 2, where the Subject ID, accession number, brief description of the subject, a bit score and e-value are listed. This list is followed by an alignment of the query and subject sequences. Each alignment indicates the percent identity and percent similarity between the two aligned sequences. Table 1 lists the ten sequences having the most significant identities.

The blastP search, Protein query-Translated db [blastP] was done using the program BLASTP 2.2.5 (version from Nov-16-2002) with the following default parameters:

- a. Databases searched: non-redundant = nr (All non-redundant GenBank CDS translations + PDB = [Sequences derived from the 3-dimensional structure from Brookhaven Protein Data Bank] + SwissProt = [Last major release of the SWISS-PROT protein sequence database (no updates)] + FIR + PRF)
- b. Limit by entrez query: No limitations were made which means all subsets of the above-cited databases were searched without any exclusions.
- c. Filter used: Low complexity. Filtering can eliminate statistically significant but biologically uninteresting reports from the blast output (e.g., hits against common acidic-, basic- or proline-rich regions), leaving the more biologically interesting regions of the query sequence available for specific matching against database sequences. Furthermore, in some cases, sequences are masked in their entirety,

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indicating that the statistical significance of any matches reported against the unfiltered query sequence should be suspect.

- d. Expect value = 10. This is the statistical significance threshold for reporting matches against database sequences. When the default value is 10, only 10 matches are expected to be found merely by chance, according to the stochastic model of Karlin and Altschul (1990). If the statistical significance ascribed to a match is greater than the EXPECT threshold, the match will not be reported. Lower EXPECT thresholds are more stringent, leading to fewer chance matches being reported. Increasing the threshold shows less stringent matches. Fractional values are acceptable.
- e. Word size = 3. This sets the size of the short regions of similarity between sequences for which BLAST initially searches.
- f. Matrix = BLOSUM62; Gap Costs: Existence = 11; Extension = 1. Here, the theory of amino acid substitution matrices is described in [1], and applied to DNA sequence comparison in [2]. In general, different substitution matrices are tailored to detecting similarities among sequences that are diverged by differing degrees [1-3]. A single matrix may nevertheless be reasonably efficient over a relatively broad range of evolutionary change [1-3]. Experimentation has shown that the BLOSUM-62 matrix [4] is among the best for detecting most weak protein similarities. For particularly long and weak alignments, the BLOSUM-45 matrix may prove superior. A detailed statistical theory for gapped alignments has not been developed, and the best gap costs to use with a given substitution matrix are determined empirically.

[1] Fitch, W.M. (1983) "Random sequences." J. Mol. Biol. 163:171-176

[2] Lipman, D.J., Wilbur, W.J., Smith T.F. & Waterman, M.S. (1984) "On the statistical significance of nucleic acid similarities." Nucl. Acids Res. 12:215-226.

[3] Altschul, S.F. & Erickson, B.W. (1985) "Significance of nucleotide sequence alignments: a method for random sequence permutation that preserves dinucleotide and codon usage." Mol. Biol. Evol. 2:526-538.

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[4] Deken, J. (1983) "Probabilistic behavior of longest-common-subsequence length." In "Time Warps, String Edits and Macromolecules: The Theory and Practice of Sequence Comparison." D. Sankoff & J.B. Kruskal (eds.), pp. 55-91, Addison-Wesley, Reading, MA.

NCBI Blast searches have for years been a routine and standard tool used by scientists for identifying similarities between sequences. The following citation from NCBI ([http://www.ncbi.nlm.nih.gov/BLAST/blast\\_overview.html](http://www.ncbi.nlm.nih.gov/BLAST/blast_overview.html)) attests to this fact: "*BLAST® (Basic Local Alignment Search Tool) is a set of similarity search programs designed to explore all of the available sequence databases regardless of whether the query is protein or DNA. The BLAST programs have been designed for speed, with a minimal sacrifice of sensitivity to distant sequence relationships. The scores assigned in a BLAST search have a well-defined statistical interpretation, making real matches easier to distinguish from random background hits. BLAST uses a heuristic algorithm which seeks local as opposed to global alignments and is therefore able to detect relationships among sequences which share only isolated regions of similarity.*"

Using the above described standard blast procedure and SEQ ID No.: 9 of the present invention as a query, I obtained the following results: The hit showing the highest degree of identity in the blastP search performed was database identification No gi 25019857 (accession XP\_110318.2). This protein is identified as being similar to hypothetical protein MGC37640 from *Mus musculus* and had a 97% sequence identity and a 97% sequence similarity. The murine LOBO protein of the present invention and XP\_110318.2 lack identity for only 16 amino acid residues. This is likely the result of, for example, irresolvable secondary structure encountered during the sequencing process. Based on this alignment, I believe that XP\_110318.2 and SEQ ID No. 9 describe one and the same sequence having equivalent functions. The nine other hits having a degree of identity greater than 70% are listed in Table 1. All of these proteins were of human or mouse origin. While the identity values for the last three sequences listed in Table 1 (Accession Nos. BAC03400.1, AAH30113.1 and XP\_237349.1) have sequence identities ranging from 88% to 91%, these sequences represent a comparison of only 128-188 amino acids of the query sequences.

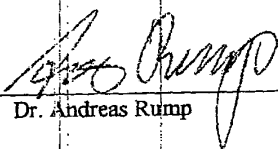
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The results of the blastP search are ordered by the value of % identity (see Table 2). The next "best" hit, after the 10 noted above, in the blastP search showed 37% identity to the protein sequence of SEQ ID NO.: 9. This next best hit in the blastP search has the identification No. gi 21292324 (equal to accession number EAA04469.1), which is defined as agCP3212 [*Anopheles gambiae* str. PEST]. The alignment of the polypeptide translated from gi 21292324 with SEQ ID NO.: 9 resulted in the value of 37% identity and accounted for 794 amino acid residues. In conclusion there are no proteins appearing in the blastP search having more than 70% identity to the amino acid sequence of SEQ ID NO.: 9 (murine LOBO protein).

All of the closest hits obtained in the blastP search, as identified in Table 1, were entered into the BLAST database after the filing date of the above-identified application. Furthermore, no function has been attributed to these sequences as illustrated by their descriptions, i.e. "hypothetical protein", etc. I believe that these proteins will have the same basic function as the murine LOBO protein given the significant degree of sequence identity and sequence similarity.

The undersigned hereby declares that all statements made herein based upon knowledge are true, and that all statements made based upon information and belief are believed to be true; and further, that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code, and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

DATED:

Feb - 27 - 2003  
Dr. Andreas Rump

Enclosures: As stated above



4-11 to #15

**Dr. Andreas Rump**  
*Curriculum vitae*

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**Personal Details**

- Date of birth: **Sept. 7, 1960**
- Place of birth: **Hamm, Germany**
- Nationality: **German**
- Family status: **married, 5 children**
- **Private Address:**  
Andreas Rump, Leutraer Weg 3a, 07745 Jena  
☎ +49-3641-212866  
✉ [andreas\\_rump@hotmail.com](mailto:andreas_rump@hotmail.com)

**Current place of work**

- **Since December 2000**  
Employed at *metaGen Pharmaceuticals*, a company dedicated to the identification of potential targets suitable for the treatment of solid tumors. Position: Scientific Leader of the "genomic technologies group"; involved in large-scale annotation of genomic DNA, cloning and expression of full-length cDNAs, DNA sequence analysis and early validation of target genes.

**Previous places of work**

- **January 1996 - November 2000 (5 years)**  
Research Scientist at the *Institute of Molecular Biotechnology (IMB)*, *Dept. of Genome Analysis*, headed by Prof. Dr. André Rosenthal. Areas of work: large-scale sequencing and molecular characterization of mouse mutants with defects in bone development.
- **July 1994 - December 1995 (1.5 years)**  
PostDoc at the *Institute of Neuropathology* in Heidelberg, headed by Prof. Dr. Marika Kiessling. Area of work: expression of glutamate receptors after global cerebral ischemia.

- **July 1991 – June 1994 (3 years)**  
PostDoc at the *German Cancer Research Center (DKFZ)* in Heidelberg.  
Department: „Interactions of carcinogens with biological macromolecules“, headed by Prof. Dr. Dr. Heinz-Walter Thielmann.  
Area of work: molecular characterization of the basal cell nevus syndrome.

#### Postgraduate education

- **July 1987 – June 1991 (4 years)**  
Ph.D. student within the *Dept. of Molecular Genetics*, at the *German National Research Center for Environment and Health (GSF)*.  
Ph.D. thesis: "Molecular characterization of the pythopathogenic fungus *Phytophthora parasitica*: construction of a representative genomic cosmid library and identification of pathologically relevant genes".

#### Undergraduate education

- **October 1980 – June 1987 (7 years)**  
Student at the Institute of Biology at the University of Bielefeld, Germany. Diploma thesis from the *Dept. of Molecular Biology and Genetics*, headed by Prof. Dr. Alfred Pühler. Title of thesis: "Nucleotide sequence of the *nifA* gene of *Klebsiella pneumoniae* M5a1".

Berlin, Feb. 21, 2003

*Andreas Rumpf*



## **Publications**

**Gene 295 (2002) 27-32**

**Different structural organization of the encephalopsin gene in man and mouse**

Kasper G, Taudien S, Staub E, Mennerich D, Rieder M, Hinzmann B, Dahl E, Schwidetzky U, Rosenthal A, **Rump A**.

**Biochem Biophys Res Comm 289 (2001) 1287-1294**

**Gene structure and regulation of the murine epithelial calcium channels ECaC1 and 2**

Weber K, Erben RG, **Rump A**, Adamski J.

**Genomics 78 (2001) 197-205**

**A high-resolution genetic, physical, and comparative gene map of the doublefoot (Dbf) region of mouse chromosome 1 and the region of conserved synteny on human chromosome 2q35**

Hayes C, **Rump A** (shared 1st authorship), Cadman MR, Harrison M, Evans EP, Lyon MF, Morriss-Kay GM, Rosenthal A, Brown SD.

**Genomics 73 (2001) 55-55**

**Complex arrangement of genes within a 220-kb region of double-duplicated DNA on human 2q37.1**

**Rump A**, Kasper G, Hayes C, Wen G, Starke H, Liehr T, Lehmann R, Lagemann D, Rosenthal A.

**Nature 409 (2001) 860-921**

**Initial sequencing and analysis of the human genome**

*Author list from IMB Jena:* Rosenthal A, Platzer M, Nyakatura G, Taudien S, **Rump A**.

**Trends in Genetics 16 (2000) 519-520**

**RUMMAGE – a high throughput sequence annotation system**

Taudien S, **Rump A**, Platzer M, Drescher B, Schattevoy R, Gloeckner G, Dette M, Baumgart C, Weber J, Menzel U, Rosenthal A.

**Cytogenet Cell Genet 91 (2000) 224-230**

**Elevated DNA sequence diversity in the genomic region of the phosphatase PPP2R3L gene in the human pseudoautosomal region**

Schiebel S, Meder J, **Rump A**, Rosenthal A, Winkelmann W, Fischer C, Rappold GA.

**Genome Res 10 (2000) 758-775**

**Comparative genome sequence analysis of the Bpa/Str region in mouse and Man**

Mallon AM, Platzer M, Bate R, Gloeckner G, Botcherby MR, Nordsiek G, Strivens MA, Kioschis P, Dangel A, Cunningham D, Straw RN, Weston P, Gilbert M, Fernando S, Goodall K, Hunter G, Greyststrong JS, Clarke D, Kimberley C, Goerdes M, Blechschmidt K, **Rump A**, Hinzmann B, Mundy CR, Miller W, Poustka A, Herman GE, Rhodes M, Denny P, Rosenthal A, Brown SD.

**Nature 405 (2000) 311-319**

**The DNA sequence of human chromosome 21. The chromosome 21 mapping and sequencing consortium**

Hattori M, Fujiyama A, Taylor TD, Watanabe H, Yada T, Park HS, Toyoda A, Ishii K, Totoki Y, Choi DK, Soeda E, Ohki M, Takagi T, Sakaki Y, Taudien S, Blechschmidt K, Polley A, Menzel U, Delabar J, Kumpf K, Lehmann R, Patterson D, Reichwald K, **Rump A**, Schillhabel M, Schudy A. et al.

**Nat Genet. 16 (1997) 54-63**

**Pseudoautosomal deletions encompassing a novel homeobox gene cause growth failure in idiopathic short stature and Turner syndrome**

Rao E, Weiss B, Fukami M, **Rump A**, Niesler B, Mertz A, Muroya K, Binder G, Kirsch S, Winkelmann M, Nordsiek G, Heinrich U, Breuning MH, Ranke MB, Rosenthal A, Ogata T, Rappold GA.

**J Cereb Blood Flow Metab 16 (1996) 1362-1365**

**Editing of GluR2 RNA in the gerbil hippocampus after global cerebral ischemia**

**Rump A**, Sommer C, Gass P, Bele S, Meissner D, Kiessling M.

**Arch Dermatol Res. 288 (1996) 399-401**

**Basal cell nevus syndrome and dysplastic nevus syndrome: investigation of gene expression by differential hybridisation**

**Rump A**, Fleischmann P, Jung EG, Werner D, Thielmann HW.

**Gene 102 (1991) 51-56**

**Tandem arrangement of tRNA(Asp)-encoding genes in Phytophthora spp.**

**Rump A**, Karlovsky P.

**J Mol Biol 203 (1988) 715-738**

**Nucleotide sequence of a 24,206-base-pair DNA fragment carrying the entire nitrogen fixation gene cluster of Klebsiella pneumoniae**

Arnold W, **Rump A**, Klipp W, Priefer UB, Pühler A.

# APPENDIX I

Alt #15

**LOBO coding sequence (CDS)-alignment: Mouse (complete) vs. Man (partial, as known at the time of patent filing)**

Region of overlap 1521 nt; Identity [:] 85.2 %

Program used: LALIGN (rigorous local alignment)

1120	1130	1140	1150	1160	1170	
MM-LOB	AAAGACTGTATCTTCACCATTGATCCATCAACTGCTCGCGACCTTGATGATGCCCTCGCC					
	.....	.....	.....	.....	.....	
HS-Lob	AAAGACTGTATCTTCACCATTGACCCATCAACCGCCCGAGACCTCGATGATGCCCTCTCC					
	10	20	30	40	50	60

1180	1190	1200	1210	1220	1230	
MM-LOB	TGCAGGCGGCTCACTGATGGCACCTTCGAAGTGGGCGTCCACATCGCCGATGTGAGTTAC					
	....	..	....	....	....	
HS-Lob	TGCAAGCCACTCGCTGACGGCAACTTCAAAGTGGGAGTTCACATTGCTGACGTGAGTTAC					
	70	80	90	100	110	120

1240	1250	1260	1270	1280	1290	
MM-LOB	TTGTTCCTGAGGGATCCTCTTTGGATAAAGTAGCTGCTGAGAGAGCCACAAGTGTCTAC					
	.....	.....	.....	.....	.....	
HS-Lob	TTGTTCCTGAGGGATCTGATCTGGATAAAGTGGCTGCCGAGAGGGCTACAAGCGTCTAC					
	130	140	150	160	170	180

1300	1310	1320	1330	1340	1350	
MM-LOB	TTGGTCCAGAAGGTGGTCCCCATGCTTCCCAGGCTTCTGTGTGAGGAAGTCTGCAGCCTC					
	.....	.....	.....	.....	.....	
HS-Lob	TTGGTTCAAAAGGTGGTCCCCATGCTTCCCAGGCTGCTGTGTGAGGAGCTGTGCAGCCTC					
	190	200	210	220	230	240

1360	1370	1380	1390	1400	1410	
MM-LOB	AACCCCATGACTGACAAGCTGACCTTCTCTGTGATCTGGAAGCTGACCCCTGAAGGCAAG					
	.....	.....	.....	.....	.....	
HS-Lob	AACCCCATGTCCGACAAGCTGACCTTCTCTGTGATCTGGACACTGACTCCAGAGGGCAAG					
	250	260	270	280	290	300

1420	1430	1440	1450	1460	1470	
MM-LOB	ATCCTTGAAGAGTGGTTTGGCCGCACTATCATCCGTTCTTGACCAAAGTACGCTACGAC					
	.....	.....	.....	.....	.....	
HS-Lob	ATCCTTGATGAATGGTTTGGCCGGACCATCATCCGCTCCTGCACCAAAGTACGCTACGAG					
	310	320	330	340	350	360

1480	1490	1500	1510	1520	1530	
MM-LOB	CATGCCCAGAGCATGATCGAAAATCCAAGTGAAGATCCCTGAGGAAGAGCTTCCCCCA					
	.....	.....	.....	.....	.....	
HS-Lob	CATGCACAGAGCATGATTGAAAGCCCAAGTGAAGAAATCCCTGCGAAAGAGCTGCCCCC					
	370	380	390	400	410	420

1540	1550	1560	1570	1580	1590	
MM-LOB	ATTTCTCCAGAGCACAGCGTCGAGGAGGTGCACCAGGCAGTCTGAACCTGCACAGCATT					
	.....	.....	.....	.....	.....	
HS-Lob	ATTTCCCAGAGCATAGCAGCGAGGAGGTACACCAGGCCGTCTTGAATCTCCACGGAATT					
	430	440	450	460	470	480

1600	1610	1620	1630	1640	1650	
MM-LOB	GCAAAGCAACTCCGCCGCCAGCGCTTTGTAGATGGCGCACTCCGTTTAGATCAGCTGAAG					
	..	.....	.....	.....	.....	
HS-Lob	GCCAAGCAGTTACGCCAGCAGCGCTTTGTGGACGGCGCACTTCGTTTGGATCAGCTAAAG					
	490	500	510	520	530	540

1660	1670	1680	1690	1700	1710
MM-LOB	CTTGCTTTTACTCTGGACCATGAGACTGGACTGCCTCAAGGATGTCACATCTATGAGTAC				
	.....				
HS-Lob	CTTGCTTTTACTCTGGACCACGAGACCGGATTGCCTCAAGGATGTCATATCTATGAGTAC				
	550	560	570	580	590 600

1720	1730	1740	1750	1760	1770
MM-LOB	CGAGACAGCAACAAGCTTGTAGAGGAGTTCATGCTCCTGGCCAACATGGCGGTGGCCCCAC				
	:: :: .....				
HS-Lob	CGCGAGAGCAACAAGCTCGTGGAGGAGTTCATGCTCTTGGCCAACATGGCAGTGGCCCCAC				
	610	620	630	640	650 660

1780	1790	1800	1810	1820	1830
MM-LOB	AAGATCTTCCGCACCTTCCCTGAGCAGGCCCTGCTGCGCCGGCATCCCCACCACAGACG				
	.....				
HS-Lob	AAGATCCACCGCGCCTTCCCCGAGCAGGCCCTGCTGCGCCGGCACCCCCCGCCCCAAACA				
	670	680	690	700	710 720

1840	1850	1860	1870	1880	1890
MM-LOB	AAGATGCTCAGTGACCTGGTGGAGTTCTGTGACCAGATGGGGCTGCCCATGGATGTCAGC				
	: .....				
HS-Lob	AGGATGCTCAGTGACCTGGTGGAAATTCTGCGACCAGATGGGGCTGCCCCTGGACTTCAGC				
	730	740	750	760	770 780

1900	1910	1920	1930	1940	1950
MM-LOB	TCTGCAGGGGCCCTAAATAAAAGCCTGACTAAGACATTTGGAGATGACAAGTACTCTCTG				
	:: ..... : .....				
HS-Lob	TCCGCAGGAGCCCTCAATAAAAGCCTGACCCAAACATTTGGAGATGACAAGTACTCACTG				
	790	800	810	820	830 840

1960	1970	1980	1990	2000	2010
MM-LOB	GCCCCGAAGGAGGTGCTCACCAACATGTACTCCCGGCCCATGCAGATGGCACTGTACTTC				
	.....				
HS-Lob	GCCCCGAAGGAGGTGCTCACCAACATGTGCTCCCGGCCCATGCAGATGGCACTGTACTTC				
	850	860	870	880	890 900

2020	2030	2040	2050	2060	2070
MM-LOB	TGCTCTGGGATGCTGCAGGACCAGGAGCAGTTCCGGCATTATGCTCTCAACGTTCCCTC				
	.....				
HS-Lob	TGCTCGGGGCTGCTGCAGGACCCAGCGCAGTTCCGGCACTACGCGCTCAATGTGCCCTG				
	910	920	930	940	950 960

2080	2090	2100	2110	2120	2130
MM-LOB	TACACACACTTCACCTCTCCCATCCGCCGCTTTGCTGACGTCATAGTGACCGCCTCCTG				
	.....				
HS-Lob	TACACACACTTCACCTCGCCCATCCGCCGCTTTGCCGACGTCCTGGTGCACCGCCTCCTG				
	970	980	990	1000	1010 1020

2140	2150	2160	2170	2180	2190
MM-LOB	GCTGCTGCTCTGGGCTACAGTGAACAGCCAGATGTGGAGCCTGATACCTACAGAAGCAA				
	.....				
HS-Lob	GCTGCCGCGTTAGGCTATAGGGAGCGACTAGACATGGCGCCCGATACCTGCAGAAACAG				
	1030	1040	1050	1060	1070 1080

2200	2210	2220	2230	2240	2250
MM-LOB	GCTGACCACTGCAATGACCGTCGCATGGCTTCCAAACGTGTGCAGGAGCTCAGCATCGGC				
	:: .....				
HS-Lob	GCGGACCACTGTAACGACCGCCGCATGGCGTCCAAGCGCGTGCAGGAGCTCAGTACCAGT				

	1090	1100	1110	1120	1130	1140
	2260	2270	2280	2290	2300	2310
MM-LOB	CTCTTCTTCG	CAGTTCTAGTAAAGGAGAGTGGCCCCCTGGAGTCCGAAGCCATGGTGATG				
HS-Lob	CTCTTCTTTGCTGTTCTGGTCAAGGAGAGTGGCCCCCTGGAGTCAGAAGCCATGGTGATG					
	1150	1160	1170	1180	1190	1200
	2320	2330	2340	2350	2360	2370
MM-LOB	GGTGTCTCTGAACCAAGCTTTCGACGTGCTGGTGCTGCGCTTTGGGGTGCAGAAAGCGCATC					
HS-Lob	GGCATCTCTGAAGCAAGCCTTCGACGTGCTGGTGCTGCGCTACGGCGTGCAGAAAGCGCATC					
	1210	1220	1230	1240	1250	1260
	2380	2390	2400	2410	2420	2430
MM-LOB	TACTGCAATGCACTGGCCCTGCGATCCTACAGCTTCCAGAAGGTGGGGAAGAAGCCAGAG					
HS-Lob	TACTGCAACGCACTGGCCCTGCGGTCCCACCACTTCCAGAAGGTGGGCAAGAAGCCGGAA					
	1270	1280	1290	1300	1310	1320
	2440	2450	2460	2470	2480	2490
MM-LOB	CTCACTCTTGTTTGGGAGCCTGATGACCTTGAAGAGGAGCCAACACAGCAGGTCATCACC					
HS-Lob	CTCACGCTGGTCTGGGAGCCTGAGGACATGGAGCAGGAGCCAGCACAGCAGGTCATCACC					
	1330	1340	1350	1360	1370	1380
	2500	2510	2520	2530	2540	2550
MM-LOB	ATCTTCAGCCTGGTGGATGTGGTCCCTGCAGGCAGAGGCCACAGCCCTCAAGTACAGTGCT					
HS-Lob	ATCTTCAGCCTGGTGGAGGTGGTCCCTGCAGGCAGAGTCCACAGCCCTCAAGTACAGCGCC					
	1390	1400	1410	1420	1430	1440
	2560	2570	2580			2590
MM-LOB	ATCCTGAAGCGACCAGGC-----CTGG-----AGAAGGCGTCT					
HS-Lob	ATCCTGAAGCGGCCAGGCACCCAGGGCCACCTGGGCCCTGAGAAGGAGGAGGAGGAGTCT					
	1450	1460	1470	1480	1490	1500
	2600	2610				
MM-LOB	GATGAGGAGCCTGAGGACTGA					
HS-Lob	GACGGTGAGCCCGAGGACTCA					
	1510	1520				

**LOBO Protein-Alignment: Mouse (complete) vs. Man (partial, as known at the time of patent filing)**

Region of overlap 506 aa; Identity [:] 88.1 %; Similarity [.] 94.8 %

Program used: LALIGN (rigorous local alignment)

```

      380      390      400      410      420      430
MM-LOB KDCIFTIDPSTARDLDDALACRRLTDGTFEVGVIADVSYFVPEGSSLDKVAAERATSVY
      .....
HS-LOB KDCIFTIDPSTARDLDDALSCKPLADGNFKVGVHIADVSYFVPEGSDLDKVAAERATSVY
      10      20      30      40      50      60

      440      450      460      470      480      490
MM-LOB LVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRRTIIRSCTKLSYD
      .....
HS-LOB LVQKVVPMLPRLLCEELCSLNPMSDKLTFSVIWTLTPEGKILDEWFGRTIIRSCTKLSYE
      70      80      90      100      110      120

      500      510      520      530      540      550
MM-LOB HAQSMIENPTEKIPPEELPPISPEHSVEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQLK
      .....
HS-LOB HAQSMIESPTEKIPAKELPPISPEHSSEEVHQAVLNLHGIKQLRQRFVDGALRLDQLK
      130      140      150      160      170      180

      560      570      580      590      600      610
MM-LOB LAFTLDHETGLPQGCHIYFYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQT
      .....
HS-LOB LAFTLDHETGLPQGCHIYFYRESNKLVEEFMLLANMAVAHKIHRAFPEQALLRRHPPPQT
      190      200      210      220      230      240

      620      630      640      650      660      670
MM-LOB KMSLDLVEFCDQMGLPMDVSSAGALNKS�TKTFGDDKYSLARKEVLTNMYSRPMQMALYF
      .....
HS-LOB RMSLDLVEFCDQMGLPVDFSSAGALNKS�TQTFGDDKYSLARKEVLTNMCSRPMQMALYF
      250      260      270      280      290      300

      680      690      700      710      720      730
MM-LOB CSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQ
      .....
HS-LOB CSGLLQDPAQFRHYALNVPLYTHFTSPIRRFADVLVHRLLAALGYRERLDMAPDTLQKQ
      310      320      330      340      350      360

      740      750      760      770      780      790
MM-LOB ADHCNDRRMASKRVQELSİGLFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRI
      .....
HS-LOB ADHCNDRRMASKRVQELSTSLFFAVLVKESGPLESEAMVMGILKQAFDVLVLRFGVQKRI
      370      380      390      400      410      420

      800      810      820      830      840      850
MM-LOB YCNALALRSYSFQKVGKKPELTLVWEPDDLEEPTQQVITIFSLVDVVLQAEATALKYSA
      .....
HS-LOB YCNALALRSHHFQKVGKKPELTLVWEPEDMEQEPQQVITIFSLVEVVLQAEATALKYSA
      430      440      450      460      470      480

      860      870
MM-LOB ILKRPGLE-----EKASDEEPED
      .....
HS-LOB ILKRPGTQGHLGPEKEEESDGEPE
      490      500
```

## APPENDIX II

**LOBO Protein-Alignment: Mouse (complete) vs. Man (complete, as determined after patent filing)**

Region of overlap 881 aa; Identity [:] 88.3 %; Similarity [.] 96.2 %

Program used: LALIGN (rigorous local alignment)

```

      10      20      30      40      50      60
MM-LOB MNHPDYKLNLRSPGTPRGVSSVVGPSAVGASPGDKKSKNKS MRGKKKSIFETYMSKEDVS
      .....
HS-LOB MSHPDYRMNLRPLGTPRGVSAVAGPHDIGASPGDKKSKNRSTRGKKKSIFETYMSKEDVS
      10      20      30      40      50      60

      70      80      90     100     110     120
MM-LOB EGLKRGTLIQGVLRINPKKFHEAFIPSPDGD R DIFIDGVVARNRALNGDLVVVKLLPEDQ
      .....
HS-LOB EGLKRGTLIQGVLRINPKKFHEAFIPSPDGD R DIFIDGVVARNRALNGDLVVVKLLPEEH
      70      80      90     100     110     120

      130     140     150     160     170
MM-LOB WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWS-GPDVIIIEAQFDDSDSEDRHG
      .....
HS-LOB WKVVKPESNDKETEAAYESDIPEELCGHHPLQQSLKSYNDSPDVIVEAQFDGSDSEDGHG
      130     140     150     160     170     180

      180     190     200     210     220     230
MM-LOB NTSG-LVDGVKKLSISTPDRGKEDSSTPVMK DENTPIPDTRGLSEKSLQKSAKVVIILE
      .....
HS-LOB ITQNVLDGVKKLSVCVSEKGREDDGAPVTKDE T TCISQDTRALSEKSLQSAKVVIILE
      190     200     210     220     230     240

      240     250     260     270     280     290
MM-LOB KKHSRAATGILKLLADKNSDLFKKYALFSPSDH RVPRIYVPLKDCPQDFMTRPKDFANTL
      .....
HS-LOB KKHSRAATGFLKLLADKNSSELFRKYALFSPSDH RVPRIYVPLKDCPQDFVARPKDYANTL
      250     260     270     280     290     300

      300     310     320     330     340     350
MM-LOB FICRIIDWKEDCNFALGQLAKSLGQAGEIEPE TEGILTEYGVDFSDFSSEVLECLPQSLP
      .....
HS-LOB FICRIVDWKEDCNFALGQLAKSLGQAGEIEPE TEGILTEYGVDFSDFSSEVLECLPQGLP
      310     320     330     340     350     360

      360     370     380     390     400     410
MM-LOB WTIPPDEVGKRRLRLKDCIFTIDPSTARDLDDA LACRRLTDGTFEVGVHIADVSYFVPEG
      .....
HS-LOB WTIPPEEFSKRRLRLKDCIFTIDPSTARDLDDA LACKPLADGNFKVGVHIADVSYFVPEG
      370     380     390     400     410     420

      420     430     440     450     460     470
MM-LOB SSLDKVAAERATSVYLVQKVVPMLPRLLCEELC SLNPMTDKLTFSVIWKLTPPEGKILEEW
      .....
HS-LOB SLDKVAERATSVYLVQKVVPMLPRLLCEELC SLNPMSTDKLTFSVIWTLTPPEGKILDEW
      430     440     450     460     470     480

      480     490     500     510     520     530
MM-LOB FGRTIIRSCTKLSYDHAQSMIENPTEKIP EELPPISPEHSVEEVHQAVLNLHSAKQLR
      .....
HS-LOB FGRTIIRSCTKLSYHAQSMIESPTEKIPAKEL PPISPEHSSEEVHQAVLNLHGIKQLR
      490     500     510     520     530     540

```

540	550	560	570	580	590
MM-LOB	RQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYERYDSNKLVEEFMLLANMAVAHKIFRT				
.....					
HS-LOB	QORFVDGALRLDQLKLAFTLDHETGLPQGCHIYERYRESNKLVEEFMLLANMAVAHKIHRA				
	550	560	570	580	590
600	610	620	630	640	650
MM-LOB	FPEQALLRRHPPPQTKMLSDLVEFCQMGPLPMDVSSAGALNKSLSLTKTFGDDKYSLARKEV				
.....					
HS-LOB	FPEQALLRRHPPPQTRMLSDLVEFCQMGPLPVDFFSSAGALNKSLSLQTFGDDKYSLARKEV				
	610	620	630	640	650
660	670	680	690	700	710
MM-LOB	LTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALG				
.....					
HS-LOB	LTNMC SRPMQMALYFCSGLLQDPAQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALG				
	670	680	690	700	710
720	730	740	750	760	770
MM-LOB	YSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVLNQ				
: . . . . .					
HS-LOB	YRERLDMAPDTLQKQADHCNDRRMASKRVQELSTSLFFAVLVKESGPLESEAMVMGILKQ				
	730	740	750	760	770
780	790	800	810	820	830
MM-LOB	AFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIFSLV				
.....					
HS-LOB	AFDVLVLRFGVQKRIYCNALALRSHHFQKVGKKPELTLVWEPEDMEQEPAAQVITIFSLV				
	790	800	810	820	830
840	850	860	870		
MM-LOB	DVVLQAEATALKYSAILKRPG-----EKASDEEPED				
.....					
HS-LOB	EVLQAEATALKYSAILKRPGTQGHGPEKEEEEESDGEPED				
	850	860	870	880	



***LOBO coding sequence (CDS)-alignment: Mouse (complete) vs. Man (complete,***  
as determined after patent filing)

Region of overlap 2646 nt; Identity [:] 85.9 %

Program used: LALIGN (rigorous local alignment)

```

              10          20          30          40          50          60
MM-LOB ATGAACCATCCTGACTACAAGCTGAACCTTCGGTCTCCGGGGACCCCCAGAGGTGTGTCC
      :::: :::::::::::::: ::::: : : ::::::::::::::::::::
HS-Lob ATGAGCCATCCTGACTACAGAATGAACCTCCGGCCCCCTGGGGACCCCCAGAGGTGTGTCT
              10          20          30          40          50          60

              70          80          90          100         110         120
MM-LOB TCTGTGGTTGGCCCGAGTGCTGTTGGTGCTTCGCCAGGTGACAAAAAGTCAAAGAACAAG
      ::::: : : : : : : : :: :::::::::::::::::::::::::::::::::::: :
HS-Lob GCTGTGGCTGGTCCACATGACATTGGTGCTTCGCCAGGTGACAAAAAGTCAAAGAACAGG
              70          80          90          100         110         120

              130         140         150         160         170         180
MM-LOB TCCATGCGAGGGAAGAAAAAGAGCATATTTGAAACCTACATGTCCAAGGAGGATGTTTCA
      :::: :::::::::::::::::::: ::::::::::::::::::::
HS-Lob TCCACACGAGGGAAGAAAAAGAGCATATTTGAAACTTACATGTCCAAGGAGGATGTTTCA
              130         140         150         160         170         180

              190         200         210         220         230         240
MM-LOB GAAGGCTTGAAGAGAGGAACACTTATCCAGGGTGTATTGAGAATCAACCCAAAGAAGTTT
      :::::::::::::::::::: :::::::::::::::::::: : ::::::::::::::
HS-Lob GAAGGCTTGAAGAGAGGAACACTCATCCAGGGTGTATTGAGAATTAATCCAAAGAAGTTT
              190         200         210         220         230         240

              250         260         270         280         290         300
MM-LOB CATGAAGCCTTCATTCCTTCTCCGGATGGTGATCGGGACATTTTATTGATGGAGTTGTT
      :::::::::::::::::::: :::::::::::::::::::: ::::::::::::::
HS-Lob CATGAAGCCTTCATTCCTTCCCCGGATGGTGATCGAGACATTTTATTGATGGGGTTGTT
              250         260         270         280         290         300

              310         320         330         340         350         360
MM-LOB GCTCGTAATAGAGCCTTAAATGGGGACCTTGTGGTTGTAAAACTGCTTCCTGAGGATCAG
      :::::::::::::::::::: :::::::::::::: : :::::::::::::: : : :
HS-Lob GCTCGTAATAGAGCCTTAAATGGGGATCTGGTGGTCGTGAAACTGCTTCCCCGAGGAGCAT
              310         320         330         340         350         360

              370         380         390         400         410         420
MM-LOB TGGAAGGCAGTTAAACCAGAGAGCAATGACAAAGAAATAGAAGCTACTTATGAAGCTGAC
      :::::::::::::::::::: :::::::::::::: : :::::::::::::: : :
HS-Lob TGGAAGGTAGTTAAACCAGAGAGCAATGACAAAGAAACAGAAGCTGCGTATGAATCAGAT
              370         380         390         400         410         420

              430         440         450         460         470
MM-LOB ATCCCTGAAGAGGGCTGTGGACATCACCCCTGCAGCAGTCCCGGAAAGGCTGGAGTG--
      ::::: : : : : : : : : : : : : : : : : : : : : : : :
HS-Lob ATCCCCGAGGAGCTCTGTGGACACCATCTCCCGCAACAGTCCCTGAAAAGCTATAATGAC
              430         440         450         460         470         480

              480         490         500         510         520         530
MM-LOB -GTCCTGATGTCATTATAGAGGCTCAGTTTGATGACAGCGACTCAGAAGATAGACATGGC
      :::::::::::::::::::: ::::::::::::::::::::
HS-Lob AGTCCTGATGTCATTGTAGAGGCTCAGTTTGATGGCAGCGACTCAGAAGATGGACATGGC
              480         490         500         510         520         530
              490         500         510         520         530         540
```

	540	550	560	570	580	590
MM-LOB	AACACC--AGTGGCCTGGTTGATGGTGTAAAGAAATTGTCAATCTCTACTCCTGACAGA					
HS-Lob	ATCACACAAAATGTGCTGGTTGATGGTGTAAAGAACTCTCAGTTTGTGTTTCTGAGAAA					
	550	560	570	580	590	600
	600	610	620	630	640	650
MM-LOB	GGAAAAGAAGATTCTAGTACTCCAGTTATGAAAGATGAGAACACCCCCATACCACAGGAC					
HS-Lob	GGAAGAGAGGATGGTGTATGCACCGGTTACAAAAGATGAGACCACCTGCATTTCACAAGAC					
	610	620	630	640	650	660
	660	670	680	690	700	710
MM-LOB	ACAAGAGGCTTATCAGAGAAGTCACTTCAGAAATCAGCAAAGGTGGTTTACATCTTGGAG					
HS-Lob	ACAAGAGCTTTATCGGAGAAATCCCTGCAAAGATCAGCAAAGGTGGTTTACATCTTGGAG					
	670	680	690	700	710	720
	720	730	740	750	760	770
MM-LOB	AAAAAGCATTCTCGAGCAGCAACTGGCATCCTGAAACTCTTGGCTGATAAGAACAGTGAC					
HS-Lob	AAAAACATTCTCGAGCAGCAACCGGCTTCCTCAAACCTCTTGGCTGATAAGAACAGCGAA					
	730	740	750	760	770	780
	780	790	800	810	820	830
MM-LOB	CTGTTTAAAGAAATACGCCCTGTTTTCTCCTTCAGACCACCGAGTACCTAGAATTTACGTA					
HS-Lob	CTGTTTAGGAAATACGCCCTGTTTTCTCCCTCAGACCACCGAGTGCCTAGAATTTATGTG					
	790	800	810	820	830	840
	840	850	860	870	880	890
MM-LOB	CCTCTCAAGGACTGTCCCCAGGACTTCATGACCCGACCTAAAGACTTTGCCAACACGCTG					
HS-Lob	CCTCTCAAGGACTGTCCCCAGGACTTTGTGGCACGGCCTAAAGATTATGCCAACACACTG					
	850	860	870	880	890	900
	900	910	920	930	940	950
MM-LOB	TTCATCTGCCGCATCATAGACTGGAAGGAGGACTGTAATTTTGCCCTGGGGCAACTGGCT					
HS-Lob	TTCATCTGCCGCATTGTGGACTGGAAGGAGGACTGCAATTTTGCCCTGGGGCAGCTGGCT					
	910	920	930	940	950	960
	960	970	980	990	1000	1010
MM-LOB	AAGAGTCTTGGGCAGGCTGGTGAAATCGAGCCTGAAACAGAAGGGATACTGACAGAATAT					
HS-Lob	AAGAGTCTTGGGCAGGCTGGTGAAATTGAGCCTGAAACAGAAGGAATACTAACAGAGTAT					
	970	980	990	1000	1010	1020
	1020	1030	1040	1050	1060	1070
MM-LOB	GGTGTGGACTTCTCTGATTTCTCTTCAGAAGTTCTTGAATGTCTCCCTCAAAGCCTGCCC					
HS-Lob	GGCGTGGATTTCTCTGATTTCTCTTCAGAAGTTCTAGAATGTCTTCCTCAAGGCCTGCCA					
	1030	1040	1050	1060	1070	1080

	1080	1090	1100	1110	1120	1130
MM-LOB	TGGACAATCCCACCTGATGAGGTGGGCAAGAGAAGAGACCTAAGGAAAGACTGTATCTTC					
	.....	.....	.....	.....	.....	.....
HS-Lob	TGGACAATTCCACCAGAGGAGTTCAGCAAGAGAAGGGATTTAAGAAAAGACTGTATCTTC					
	1090	1100	1110	1120	1130	1140

	1140	1150	1160	1170	1180	1190
MM-LOB	ACCATTGATCCATCAACTGCTCGCGACCTTGATGATGCCCTCGCCTGCAGGCGGCTCACT					
	.....	.....	.....	.....	.....	.....
HS-Lob	ACCATTGACCCATCAACCGCCCGAGACCTCGATGATGCCCTCTCCTGCAAGCCACTCGCT					
	1150	1160	1170	1180	1190	1200

	1200	1210	1220	1230	1240	1250
MM-LOB	GATGGCACCTTCGAAGTGGGCGTCCACATCGCCGATGTGAGTTACTTTGTTCTGAGGGA					
	..	..	..	..	..	..
HS-Lob	GACGGCAACTTCAAAGTGGGAGTTCACATTGCTGACGTGAGTTACTTTGTTCCGGAGGGA					
	1210	1220	1230	1240	1250	1260

	1260	1270	1280	1290	1300	1310
MM-LOB	TCCTCTTTGGATAAAGTAGCTGCTGAGAGAGCCACAAGTGTCTACTTGGTCCAGAAGGTG					
	..	:	.....	.....	.....	.....
HS-Lob	TCTGATCTGGATAAAGTGGCTGCCGAGAGGGCTACAAGCGTCTACTTGGTTCAAAGGTG					
	1270	1280	1290	1300	1310	1320

	1320	1330	1340	1350	1360	1370
MM-LOB	GTCCCCATGCTTCCCAGGCTTCTGTGTGAGGAACTCTGCAGCCTCAACCCCATGACTGAC					
	.....	.....	.....	.....	.....	.....
HS-Lob	GTCCCCATGCTTCCCAGGCTGCTGTGTGAGGAGCTGTGCAGCCTCAACCCCATGTCCGAC					
	1330	1340	1350	1360	1370	1380

	1380	1390	1400	1410	1420	1430
MM-LOB	AAGCTGACCTTCTCTGTGATCTGGAAGCTGACCCCTGAAGGCAAGATCCTTGAAGAGTGG					
	.....	.....	.....	.....	.....	.....
HS-Lob	AAGCTGACCTTCTCTGTGATCTGGACACTGACTCCAGAGGGCAAGATCCTTGATGAATGG					
	1390	1400	1410	1420	1430	1440

	1440	1450	1460	1470	1480	1490
MM-LOB	TTTGGCCGCACTATCATCCGTTCTTGCACCAAAGTACGAGCTACGACCATGCCCAGAGCATG					
	.....	..	.....	.....	.....	.....
HS-Lob	TTTGGCCGGACCATCATCCGCTCCTGCACCAAAGTACGAGCTACGAGCATGCACAGAGCATG					
	1450	1460	1470	1480	1490	1500

	1500	1510	1520	1530	1540	1550
MM-LOB	ATCGAAAATCCAAGTGAAGATCCCTGAGGAAGAGCTTCCCCAATTTCTCCAGAGCAC					
	..	.....	.....	.....	.....	.....
HS-Lob	ATTGAAAGCCCAACTGAGAAAATCCCTGCGAAAGAGCTGCCCCCATTTCGCCAGAGCAT					
	1510	1520	1530	1540	1550	1560

	1560	1570	1580	1590	1600	1610
MM-LOB	AGCGTCGAGGAGGTGCACCAGGCAGTCCCTGAACCTGCACAGCATTGCAAAGCAACTCCGC					
	...	.....	.....	.....	.....	.....
HS-Lob	AGCAGCGAGGAGGTACACCAGGCCGTCTTGAATCTCCACGGAATTGCCAAGCAGTTACGC					
	1570	1580	1590	1600	1610	1620

	1620	1630	1640	1650	1660	1670
MM-LOB	CGCCAGCGCTTTGTAGATGGCGCACTCCGTTTAGATCAGCTGAAGCTTGCTTTTACTCTG					
	:	.....	.....	.....	.....	.....
HS-Lob	CAGCAGCGCTTTGTGGACGGCGCACTTCGTTTGGATCAGCTAAAGCTTGCTTTTCACTCTG					
	1630	1640	1650	1660	1670	1680

	1680	1690	1700	1710	1720	1730
MM-LOB	GACCATGAGACTGGACTGCCTCAAGGATGTCACATCTATGAGTACCGAGACAGCAACAAG					
HS-Lob	GACCACGAGACCGGATTGCCTCAAGGATGTCATATCTATGAGTACCGCGAGAGCAACAAG					
	1690	1700	1710	1720	1730	1740
	1740	1750	1760	1770	1780	1790
MM-LOB	CTTG TAGAGGAGTT CATGCTCCTGGCCAACATGGCGGTGGCCCACAAGATCTTCCGCACC					
HS-Lob	CTCGTGGAGGAGTT CATGCTCTTGCCAACATGGCAGTGGCCCACAAGATCCACCGCGCC					
	1750	1760	1770	1780	1790	1800
	1800	1810	1820	1830	1840	1850
MM-LOB	TTCCCTGAGCAGGCCCTGCTGCGCCGGCATCCCCACCACAGACGAAGATGCTCAGTGAC					
HS-Lob	TTCCCCGAGCAGGCCCTGCTGCGCCGGCACCCCCGCCCAAACAAGGATGCTCAGTGAC					
	1810	1820	1830	1840	1850	1860
	1860	1870	1880	1890	1900	1910
MM-LOB	CTGGTGGAGTTCTGTGACCAGATGGGGCTGCCCATGGATGTCAGCTCTGCAGGGGCCCTA					
HS-Lob	CTGGTGGAAATTCTGCGACCAGATGGGGCTGCCCGTGGACTTCAGCTCCGCAGGAGCCCTC					
	1870	1880	1890	1900	1910	1920
	1920	1930	1940	1950	1960	1970
MM-LOB	AATAAAAGCCTGACTAAGACATTTGGAGATGACAAGTACTCTCTGGCCCGGAAGGAGGTG					
HS-Lob	AATAAAAGCCTGACCCAAACATTTGGAGATGACAAGTACTCACTGGCCCGCAAGGAGGTG					
	1930	1940	1950	1960	1970	1980
	1980	1990	2000	2010	2020	2030
MM-LOB	CTCACCAACATGTACTCCCGGCCCATGCAGATGGCACTGTACTTCTGCTCTGGGATGCTG					
HS-Lob	CTCACCAACATGTGCTCCCGGCCCATGCAGATGGCACTGTACTTCTGCTCGGGGCTGCTG					
	1990	2000	2010	2020	2030	2040
	2040	2050	2060	2070	2080	2090
MM-LOB	CAGGACCAGGAGCAGTTCCGGCATTATGCTCTCAACGTTCCCTCTACACACACTTCACC					
HS-Lob	CAGGACCCAGCGCAGTTCCGGCACTACGCGCTCAATGTGCCCTGTACACACACTTCACC					
	2050	2060	2070	2080	2090	2100
	2100	2110	2120	2130	2140	2150
MM-LOB	TCTCCCATCCGCCGCTTTGCTGACGTCATAGTGACCGCCTCCTGGCTGCTGCTCTGGGC					
HS-Lob	TCGCCCATCCGCCGCTTTGCCGACGTCCTGGTGACCGCCTCCTGGCTGCCGCGTTAGGC					
	2110	2120	2130	2140	2150	2160
	2160	2170	2180	2190	2200	2210
MM-LOB	TACAGTGAACAGCCAGATGTGGAGCCTGATACCCTACAGAAGCAAGCTGACCACTGCAAT					
HS-Lob	TATAGGGAGCGACTAGACATGGCGCCCCGATACCCTGCAGAAACAGGCGGACCACTGTAAC					
	2170	2180	2190	2200	2210	2220

	2220	2230	2240	2250	2260	2270
MM-LOB	GACCGTCGCATGGCTTCCAAACGTGTGCAGGAGCTCAGCATCGGCCTCTTCTTCGCAGTT					
	::::	::::	::::	::::	::::	::::
HS-Lob	GACCGCCGCATGGCGTCCAAGCGCGTGCAGGAGCTCAGTACCAGTCTCTTCTTTGCTGTT					
	2230	2240	2250	2260	2270	2280

	2280	2290	2300	2310	2320	2330
MM-LOB	CTAGTAAAGGAGAGTGGCCCCCTGGAGTCCGAAGCCATGGTGATGGGTGTCCTGAACCAA					
	::	::	::::	::::	::::	::::
HS-Lob	CTGGTCAAGGAGAGTGGCCCCCTGGAGTCCGAAGCCATGGTGATGGGCATCCTGAAGCAA					
	2290	2300	2310	2320	2330	2340

	2340	2350	2360	2370	2380	2390
MM-LOB	GCTTTCGACGTGCTGGTGCTGCGCTTTGGGGTGCAGAAGCGCATCTACTGCAATGCACTG					
	::	::::	::::	::::	::::	::::
HS-Lob	GCCTTCGACGTGCTGGTGCTGCGCTACGGCGTGCAGAAGCGCATCTACTGCAACGCACTG					
	2350	2360	2370	2380	2390	2400

	2400	2410	2420	2430	2440	2450
MM-LOB	GCCCTGCGATCCTACAGCTTCCAGAAGGTGGGAAGAAGCCAGAGCTCACTCTTGTTTGG					
	::::	::	::::	::::	::::	::::
HS-Lob	GCCCTGCGGTCCCACCACTTCCAGAAGGTGGGAAGAAGCCGGAACACGCTGGTCTGG					
	2410	2420	2430	2440	2450	2460

	2460	2470	2480	2490	2500	2510
MM-LOB	GAGCCTGATGACCTTGAAGAGGAGCCAACACAGCAGGTCATCACCATCTTCAGCCTGGTG					
	::::	::	::::	::::	::::	::::
HS-Lob	GAGCCTGAGGACATGGAGCAGGAGCCAGCACAGCAGGTCATCACCATCTTCAGCCTGGTG					
	2470	2480	2490	2500	2510	2520

	2520	2530	2540	2550	2560	2570
MM-LOB	GATGTGGTCTCTGCAGGCAGAGGCCACAGCCCTCAAGTACAGTGCTATCCTGAAGCGACCA					
	::	::::	::::	::::	::::	::::
HS-Lob	GAGGTGGTCTCTGCAGGCAGAGTCCACAGCCCTCAAGTACAGCGCCATCCTGAAGCGGCCA					
	2530	2540	2550	2560	2570	2580

		2580		2590	2600
MM-LOB	GGC-----CTGG-----AGAAGGCGTCTGATGAGGAGCCTGAG				
	::	::::	::	::::	::::
HS-Lob	GGCACCCAGGGCCACCTGGGCCCTGAGAAGGAGGAGGAGTCTGACGGTGAGCCCCGAG				
	2590	2600	2610	2620	2640

	2610
MM-LOB	GACTGA
	::::
HS-Lob	GACTCA

TABLE 1

Blast of **complete mouse LOBO** protein against translated GenBank produced hits with significant similarity with the following DB-entries (Blast performed 30-Jan-2003):

All other matches were significantly lower than 70 % aa identity

RESULT: no entry with significant (i.e. >70 % aa identity) was older than May 2002 !!

Similarity	Accession	Entry date	Remark
818/870 (94%)	NP_705758.1	26-JAN-2003	
801/831 (96%)	BAC27292.1	05-DEC-2002	
720/772 (93%)	XP_129937.2	16-NOV-2002	version 1: 08-OCT-2002
647/663 (97%)	XP_110318.2	15-NOV-2002	version 1: 30-APR-2002
569/590 (96%)	BAC26549.1	05-DEC-2002	
451/532 (84%)	AAH36113.1	23-SEP-2002	
410/527 (77%)	BAC04324.1	15-JUL-2002	
167/188 (88%)	BAC03400.1	15-JUL-2002	
119/135 (88%)	AAH30113.1	20-MAY-2002	
117/128 (91%)	XP_237349.1	28-JAN-2003	

TABLE 2

The detailed Blast results are as follows:

BLASTP 2.2.5 [version from Nov-16-2002]

Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

RID: 1043949663-07491-641

Query= MM-LOBO 871 bp PROT 6-NOV-1998,  
871 bases, 670 checksum.  
(870 letters)

Database: All non-redundant GenBank CDS  
translations+PDB+SwissProt+PIR+PRF  
1,321,324 sequences; 423,161,544 total letters

Sequences producing significant alignments:				Score (bits)	E Value
gi 24233556 ref NP_705758.1	RIKEN cDNA 4930429A22; hypothe...	1640	0.0		
gi 26327097 dbj BAC27292.1	unnamed protein product [Mus mu...	1605	0.0		
gi 25047588 ref XP_129937.2	hypothetical protein MGC37640 ...	1453	0.0		
gi 25019857 ref XP_110318.2	similar to hypothetical protei...	1303	0.0		
gi 26325590 dbj BAC26549.1	unnamed protein product [Mus mu...	1166	0.0		
gi 23271317 gb AAH36113.1	Unknown (protein for MGC:33943) ...	916	0.0		
gi 21753324 dbj BAC04324.1	unnamed protein product [Homo s...	812	0.0		
gi 21292324 gb EAA04469.1	agCP3212 [Anopheles gambiae str....	424	e-117		
gi 19115422 ref NP_594510.1	ribonuclease II RNB family pro...	418	e-115		
gi 15220899 ref NP_177891.1	putative 3'-5' exoribonuclease...	414	e-114		

gi	25406521	pir	E96806	hypothetical protein T32E8.1 [impor...	402	e-110
gi	25332397	pir	A84553	probable mitotic control protein di...	396	e-109
gi	24654592	ref	NP_728490.1	CG16940-PC [Drosophila melanog...	367	e-100
gi	19922976	ref	NP_612012.1	CG16940-PA [Drosophila melanog...	367	e-100
gi	15292611	gb	AAK93574.1	SD10981p [Drosophila melanogaster]	351	2e-95
gi	18488261	ref	XP_081229.1	Dis3 [Drosophila melanogaster]...	350	6e-95
gi	21748526	dbj	BAC03400.1	FLJ00327 protein [Homo sapiens]	343	9e-93
gi	26327903	dbj	BAC27692.1	unnamed protein product [Mus mu...	340	7e-92
gi	13446610	emb	CAC35051.1	putative exoribonuclease DIS3 [...	335	2e-90
gi	5262619	emb	CAB45749.1	hypothetical protein [Homo sapiens]	334	4e-90
gi	27703387	ref	XP_224449.1	similar to mitotic control pro...	330	7e-89
gi	19923416	ref	NP_055768.2	mitotic control protein dis3 h...	330	7e-89
gi	6324552	ref	NP_014621.1	Possible component of RCC1-Ran ...	321	3e-86
gi	21297331	gb	EAA09476.1	ebiP3704 [Anopheles gambiae str....	313	6e-84
gi	14250908	emb	CAC39259.1	Rrp44p homologue [Trypanosoma b...	313	1e-83
gi	19113445	ref	NP_596653.1	mitotic control protein dis3 [...	301	4e-80
gi	15021874	dbj	BAB62212.1	hypothetical protein [Macaca fa...	291	3e-77
gi	19115966	ref	NP_588616.1	hypothetical protein MGC4562 [...	284	4e-75
gi	18916779	dbj	BAB85541.1	KIAA1955 protein [Homo sapiens]	284	5e-75
gi	27369724	ref	NP_766107.1	hypothetical protein 4932411M1...	283	9e-75
gi	14250916	emb	CAC39263.1	putative ribonuclease II-like p...	278	4e-73
gi	15559519	gb	AAH14124.1	AAH14124 Unknown (protein for IMA...	270	1e-70
gi	23136616	gb	ZP_00118334.1	hypothetical protein [Cytopha...	265	3e-69
gi	19173030	ref	NP_597581.1	similarity to DIS3 PROTEIN (RN...	260	6e-68
gi	7493807	pir	T30524	protein phosphatase Ssd1 homolog - y...	246	1e-63
gi	22748821	ref	NP_689596.1	hypothetical protein MGC42174 ...	242	2e-62
gi	27685983	ref	XP_237349.1	similar to hypothetical protei...	241	5e-62
gi	6320499	ref	NP_010579.1	Product of gene unknown; Ssdip ...	221	3e-56
gi	15616115	ref	NP_244420.1	ribonuclease R; virulence-asso...	214	5e-54
gi	23099883	ref	NP_693349.1	ribonuclease R [Oceanobacillus ...	209	1e-52
gi	21673344	ref	NP_661409.1	ribonuclease II family protein...	208	4e-52
gi	15672924	ref	NP_267098.1	ribonuclease [Lactococcus lact...	206	9e-52
gi	21754656	dbj	BAC04542.1	unnamed protein product [Homo s...	205	3e-51
gi	23020108	gb	ZP_00059814.1	hypothetical protein [Clostri...	203	1e-50
gi	16801605	ref	NP_471873.1	similar to exoribonuclease RNA...	201	3e-50
gi	16804487	ref	NP_465972.1	similar to exoribonuclease RNA...	200	7e-50
gi	21397569	ref	NP_653554.1	RNB, RNB-like protein [Bacillu...	197	7e-49
gi	16080414	ref	NP_391241.1	similar to hypothetical protei...	195	3e-48
gi	15894003	ref	NP_347352.1	FUSION ribonuclease and riboso...	190	7e-47
gi	27467483	ref	NP_764120.1	ribonuclease R [Staphylococcus...	190	8e-47
gi	24379988	ref	NP_721943.1	putative exoribonuclease R (RN...	190	1e-46
gi	19113103	ref	NP_596311.1	hypothetical protein; ribonucl...	188	3e-46
gi	21282471	ref	NP_645559.1	ribonuclease R [Staphylococcus...	187	7e-46
gi	15923770	ref	NP_371304.1	conserved hypothetical protein...	186	1e-45
gi	27685919	ref	XP_217466.1	similar to hypothetical protei...	186	2e-45
gi	6473411	dbj	BAA87129.1	Hypothetical protein [Schizosacc...	186	2e-45
gi	15926457	ref	NP_373990.1	ribonuclease R [Staphylococcus...	185	3e-45
gi	19745621	ref	NP_606757.1	putative exoribonuclease R [St...	185	3e-45
gi	15674608	ref	NP_268782.1	putative exoribonuclease R [St...	184	6e-45
gi	21909888	ref	NP_664156.1	putative exoribonuclease R [St...	183	9e-45
gi	25011590	ref	NP_735985.1	Unknown [Streptococcus agalact...	183	1e-44
gi	27685993	ref	XP_237351.1	similar to hypothetical protei...	183	1e-44
gi	22537625	ref	NP_688476.1	exoribonuclease, VacB/Rnb fami...	183	1e-44
gi	15902922	ref	NP_358472.1	Exoribonuclease R [Streptococc...	182	2e-44
gi	15900852	ref	NP_345456.1	exoribonuclease, VacB/Rnb fami...	181	3e-44
gi	15673187	ref	NP_267361.1	ribonuclease [Lactococcus lact...	179	1e-43
gi	15805382	ref	NP_294076.1	ribonuclease [Deinococcus radi...	176	2e-42
gi	15605122	ref	NP_219907.1	Ribonuclease Family [Chlamydia...	172	3e-41
gi	15618415	ref	NP_224700.1	ribonuclease family [Chlamydo...	170	1e-40
gi	20807463	ref	NP_622634.1	Exoribonucleases [Thermoanaero...	169	2e-40
gi	23024105	gb	ZP_00063328.1	hypothetical protein [Leucono...	169	2e-40
gi	27380223	ref	NP_771752.1	exoribonuclease [Bradyrhizobiu...	167	6e-40
gi	15835291	ref	NP_297050.1	exoribonuclease, VacB/Rnb fami...	167	9e-40
gi	23053471	gb	ZP_00079680.1	hypothetical protein [Geobact...	166	2e-39
gi	20881074	ref	XP_127907.1	RIKEN cDNA 2810028N01 [Mus mus...	163	1e-38

gi 20071792 gb AAH27357.1	Similar to mitotic control prote...	163	1e-38
gi 15643485 ref NP_228531.1	vacB protein [Thermotoga marit...	162	2e-38
gi 23467938 gb ZP_00123514.1	hypothetical protein [Haemoph...	161	4e-38
gi 15607021 ref NP_214403.1	VacB protein (ribonuclease II ...	160	7e-38
gi 19703943 ref NP_603505.1	Exoribonuclease II [Fusobacter...	160	8e-38
gi 18310278 ref NP_562212.1	ribonuclease R [Clostridium pe...	160	1e-37
gi 23038196 gb ZP_00070371.1	hypothetical protein [Oenococ...	159	1e-37
gi 15642594 ref NP_232227.1	ribonuclease R [Vibrio cholera...	159	2e-37
gi 17545947 ref NP_519349.1	PROBABLE EXORIBONUCLEASE RNASE...	158	5e-37
gi 22995402 gb ZP_00039879.1	hypothetical protein [Xylella...	157	8e-37
gi 16763187 ref NP_458804.1	ribonuclease R (RNase R) [Salm...	157	8e-37
gi 22954374 gb ZP_00002175.1	hypothetical protein [Nitroso...	156	1e-36
gi 16132001 ref NP_418600.1	putative enzyme [Escherichia c...	156	1e-36
gi 15804768 ref NP_290809.1	putative enzyme [Escherichia c...	156	1e-36
gi 731093 sp P21499 RNR_EC0LI	Ribonuclease R (RNase R) (Vac...	156	1e-36
gi 391901 dbj BAA01777.1	ORF-2 [Shigella flexneri]	155	2e-36
gi 24115534 ref NP_710044.1	putative enzyme [Shigella flex...	155	2e-36
gi 27735249 sp P30851 RNR_SHIFL	Ribonuclease R (RNase R) (V...	155	2e-36
gi 26553786 ref NP_757720.1	3'-5' exoribonuclease RNase R ...	155	2e-36
gi 27364704 ref NP_760232.1	Exoribonuclease R [Vibrio vuln...	154	5e-36
gi 21242317 ref NP_641899.1	RNase R [Xanthomonas axonopodi...	154	5e-36
gi 15600130 ref NP_253624.1	exoribonuclease RNase R [Pseud...	154	5e-36
gi 23003758 gb ZP_00047408.1	hypothetical protein [Lactoba...	154	6e-36
gi 26251071 ref NP_757111.1	Ribonuclease R [Escherichia co...	154	6e-36
gi 11359056 pir T45283	growth polarity maintenance protein...	154	7e-36

#### Alignments

>gi|24233556|ref|NP\_705758.1| RIKEN cDNA 4930429A22; hypothetical protein MGC37640 [Mus musculus]  
gi|23273603|gb|AAH36177.1| Unknown (protein for MGC:37640) [Mus musculus]  
Length = 870

Score = 1640 bits (4247), Expect = 0.0  
Identities = 818/870 (94%), Positives = 818/870 (94%)

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Query: 1  MNHPDYKLNLRXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXIFETYMSKEDVS 60
          MNHPDYKLNLR                                     D             IFETYMSKEDVS
Sbjct: 1  MNHPDYKLNLRSPGTPRGVSSVVGPSAVGASPGDKKSKNKS MRGKKKSIFETYMSKEDVS 60

Query: 61  EGLKRGTLIQGVLRLINPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120
          EGLKRGTLIQGVLRLINPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDLVVVKLLPEDQ
Sbjct: 61  EGLKRGTLIQGVLRLINPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120

Query: 121  WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQFDDSDSEDRHGN 180
          WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQFDDSDSEDRHGN
Sbjct: 121  WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQFDDSDSEDRHGN 180

Query: 181  TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAKVVIIEKK 240
          TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAKVVIIEKK
Sbjct: 181  TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAKVVIIEKK 240

Query: 241  HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFI 300
          HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFI
Sbjct: 241  HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFI 300

Query: 301  CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWT 360
          CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWT
Sbjct: 301  CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWT 360

Query: 361  IPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSS 420
          IPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSS
Sbjct: 361  IPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSS 420

Query: 421  LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWF 480

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LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFG  
 Sbjct: 421 LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFG 480

Query: 481 RTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHLSIAKQLRRQ 540  
 RTIIRSCTKLSYDHAQSMIEN HSVEEVHQAVLNLHLSIAKQLRRQ

Sbjct: 481 RTIIRSCTKLSYDHAQSMIENPTEKIPPEELPPISPEHSVEEVHQAVLNLHLSIAKQLRRQ 540

Query: 541 RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600  
 RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP

Sbjct: 541 RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600

Query: 601 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLT 660  
 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLT

Sbjct: 601 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLT 660

Query: 661 NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLAAALGYS 720  
 NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLAAALGYS

Sbjct: 661 NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLAAALGYS 720

Query: 721 EQPDVEPDTLQKQADHCNDRRMASKRVQELS IGLFFAVLVKESGPLESEAMVMGVNLQAF 780  
 EQPDVEPDTLQKQADHCNDRRMASKRVQELS IGLFFAVLVKESGPLESEAMVMGVNLQAF

Sbjct: 721 EQPDVEPDTLQKQADHCNDRRMASKRVQELS IGLFFAVLVKESGPLESEAMVMGVNLQAF 780

Query: 781 DVLVLRFGVQKRIYCNALALRSYSFQVKGKPELTLVWEPDDLEEEPTQQVITIFSLVDV 840  
 DVLVLRFGVQKRIYCNALALRSYSFQVKGKPELTLVWEPDDLEEEPTQQVITIFSLVDV

Sbjct: 781 DVLVLRFGVQKRIYCNALALRSYSFQVKGKPELTLVWEPDDLEEEPTQQVITIFSLVDV 840

Query: 841 VLQAEATALKYSAILKRPGLEKASDEEPED 870  
 VLQAEATALKYSAILKRPGLEKASDEEPED

Sbjct: 841 VLQAEATALKYSAILKRPGLEKASDEEPED 870

>gi|26327097|dbj|BAC27292.1| unnamed protein product [Mus musculus]  
 Length = 831

Score = 1605 bits (4155), Expect = 0.0  
 Identities = 801/831 (96%), Positives = 801/831 (96%), Gaps = 14/831 (1%)

Query: 54 MSKEDVSEGLKRGTLIQGVLRLNPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDLVVV 113  
 MSKEDVSEGLKRGTLIQGVLRLNPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDLVVV

Sbjct: 1 MSKEDVSEGLKRGTLIQGVLRLNPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDLVVV 60

Query: 114 KLLPEDQWK-----AVKPESNDKEI EATYEADIPEEGCGHHPLQQSRKGWS 159  
 KLLPEDQWK AVKPESNDKEI EATYEADIPEEGCGHHPLQQSRKGWS

Sbjct: 61 KLLPEDQWKPRITLSLPGVLGLQAVKPESNDKEI EATYEADIPEEGCGHHPLQQSRKGWS 120

Query: 160 GPDVIIIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPI PQDT 219  
 GPDVIIIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPI PQDT

Sbjct: 121 GPDVIIIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPI PQDT 180

Query: 220 RGLSEKSLQSAKV VVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVP 279  
 RGLSEKSLQSAKV VVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVP

Sbjct: 181 RGLSEKSLQSAKV VVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVP 240

Query: 280 LKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYG 339  
 LKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYG

Sbjct: 241 LKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYG 300

Query: 340 VDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTD 399  
 VDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTD

Sbjct: 301 VDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTD 360

Query: 400 GTFEVG VHIADVSYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDK 459  
 GTFEVG VHIADVSYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDK

Sbjct: 361 GTFEVG VHIADVSYFVPEGSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDK 420

Query: 460 LTFSVIWKLTPGKILEEWFGRTIIR SCKLSYDHAQSMIENXXXXXXXXXXXXXXXXXXXXHS 519  
 LTFSVIWKLTPGKILEEWFGRTIIR SCKLSYDHAQSMIEN HS  
 Sbjct: 421 LTFSVIWKLTPGKILEEWFGRTIIR SCKLSYDHAQSMIENPTEKIPEEELPPISPEHS 480

Query: 520 VEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKL 579  
 VEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKL  
 Sbjct: 481 VEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKL 540

Query: 580 VEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALN 639  
 VEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALN  
 Sbjct: 541 VEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALN 600

Query: 640 KSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTS 699  
 KSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTS  
 Sbjct: 601 KSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTS 660

Query: 700 PIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVL 759  
 PIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVL  
 Sbjct: 661 PIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVL 720

Query: 760 VKESGPLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWE 819  
 VKESGPLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWE  
 Sbjct: 721 VKESGPLESEAMVMGVLNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWE 780

Query: 820 PDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLEKASDEEPED 870  
 PDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLEKASDEEPED  
 Sbjct: 781 PDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLEKASDEEPED 831

>gi|25047588|ref|XP\_129937.2| hypothetical protein MGC37640 [Mus musculus]  
 Length = 819

Score = 1453 bits (3762), Expect = 0.0  
 Identities = 720/772 (93%), Positives = 720/772 (93%)

Query: 1 MNHPDYKLNLRXXXXXXXXXXXXXXXXXXXXDXXXXXXXXXXXXXXXXXIFETYMSKEDVS 60  
 MNHPDYKLNLR D IFETYMSKEDVS  
 Sbjct: 1 MNHPDYKLNLRSPGTPRGVSSVVGPSAVGASPGDKKSKNKS MRGKKKSIFETYMSKEDVS 60

Query: 61 EGLKRGTLIQGVLRLNPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120  
 EGLKRGTLIQGVLRLNPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ  
 Sbjct: 61 EGLKRGTLIQGVLRLNPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIIEAQFDDSDSEDRHGN 180  
 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIIEAQFDDSDSEDRHGN  
 Sbjct: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIIEAQFDDSDSEDRHGN 180

Query: 181 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQSAKVVIILEKK 240  
 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQSAKVVIILEKK  
 Sbjct: 181 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQSAKVVIILEKK 240

Query: 241 HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPDQDFMTRPKDFANTLFI 300  
 HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPDQDFMTRPKDFANTLFI  
 Sbjct: 241 HSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPDQDFMTRPKDFANTLFI 300

Query: 301 CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWT 360  
 CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWT  
 Sbjct: 301 CRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWT 360

Query: 361 IPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSS 420  
 IPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSS  
 Sbjct: 361 IPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSS 420

Query: 421 LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWFG 480  
 LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWFG  
 Sbjct: 421 LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWFG 480

Query: 481 RTIIRSECTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQ 540  
RTIIRSECTKLSYDHAQSMIEN HSVEEVHQAVLNLSIAKQLRRQ  
Sbjct: 481 RTIIRSECTKLSYDHAQSMIENPTEKIPEEELPPISPEHSVEEVHQAVLNLSIAKQLRRQ 540

Query: 541 RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600  
RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP  
Sbjct: 541 RFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600

Query: 601 EQALLRRHPPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLT 660  
EQALLRRHPPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLT  
Sbjct: 601 EQALLRRHPPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLT 660

Query: 661 NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLAAALGYS 720  
NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLAAALGYS  
Sbjct: 661 NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLAAALGYS 720

Query: 721 EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMV 772  
EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMV  
Sbjct: 721 EQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMV 772

>gi|25019857|ref|XP\_110318.2| similar to hypothetical protein MGC37640 [Mus musculus]  
Length = 663

Score = 1303 bits (3371), Expect = 0.0  
Identities = 647/663 (97%), Positives = 647/663 (97%)

Query: 208 MKDENTPIPDTRGLSEKSLQSAKVVIILEKKHSRAATGILKLLADKNSDLFKKYALFS 267  
MKDENTPIPDTRGLSEKSLQSAKVVIILEKKHSRAATGILKLLADKNSDLFKKYALFS  
Sbjct: 1 MKDENTPIPDTRGLSEKSLQSAKVVIILEKKHSRAATGILKLLADKNSDLFKKYALFS 60

Query: 268 PSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI 327  
PSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI  
Sbjct: 61 PSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI 120

Query: 328 EPETEGILTEYGVDVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD 387  
EPETEGILTEYGVDVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD  
Sbjct: 121 EPETEGILTEYGVDVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD 180

Query: 388 LDDALACRRLTDGTTFEYGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLC 447  
LDDALACRRLTDGTTFEYGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLC  
Sbjct: 181 LDDALACRRLTDGTTFEYGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLC 240

Query: 448 EELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRTIIRSECTKLSYDHAQSMIENXXXXXX 507  
EELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRTIIRSECTKLSYDHAQSMIEN  
Sbjct: 241 EELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRTIIRSECTKLSYDHAQSMIENPTEKIP 300

Query: 508 XXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQG 567  
HSVEEVHQAVLNLSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQG  
Sbjct: 301 EEELPPISPEHSVEEVHQAVLNLSIAKQLRRQRFDGALRLDQLKLAFTLDHETGLPQG 360

Query: 568 CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPPQTKMLSDLVEFCDQMG 627  
CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPPQTKMLSDLVEFCDQMG  
Sbjct: 361 CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPPQTKMLSDLVEFCDQMG 420

Query: 628 LPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHY 687  
LPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHY  
Sbjct: 421 LPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHY 480

Query: 688 ALNVPLYTHFTSPIRRFADVIVHRLAAALGYSEQPDVEPDTLQKQADHCNDRRMASKRV 747  
ALNVPLYTHFTSPIRRFADVIVHRLAAALGYSEQPDVEPDTLQKQADHCNDRRMASKRV  
Sbjct: 481 ALNVPLYTHFTSPIRRFADVIVHRLAAALGYSEQPDVEPDTLQKQADHCNDRRMASKRV 540

Query: 748 QELSIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQK 807

QELSIGLFFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQK  
 Sbjct: 541 QELSIGLFFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQK 600

Query: 808 VGKKPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLKASDEE 867  
 VGKKPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLKASDEE  
 Sbjct: 601 VGKKPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKRPGLKASDEE 660

Query: 868 PED 870  
 PED  
 Sbjct: 661 PED 663

>gi|26325590|dbj|BAC26549.1| unnamed protein product [Mus musculus]  
 Length = 684

Score = 1166 bits (3016), Expect = 0.0  
 Identities = 569/590 (96%), Positives = 570/590 (96%)

Query: 150 PLQQSRKGWSPDVIIIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMK 209  
 P +RKGWSPDVIIIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMK  
 Sbjct: 14 PCSSARKGWSPDVIIIEAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMK 73

Query: 210 DENTPIPDTRGLSEKSLQKSAKVVIIEKKHSRAATGILKLLADKNSDLFKKYALFSPS 269  
 DENTPIPDTRGLSEKSLQKSAKVVIIEKKHSRAATGILKLLADKNSDLFKKYALFSPS  
 Sbjct: 74 DENTPIPDTRGLSEKSLQKSAKVVIIEKKHSRAATGILKLLADKNSDLFKKYALFSPS 133

Query: 270 DHRVPRIYVPLKDCPDQFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEP 329  
 DHRVPRIYVPLKDCPDQFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEP  
 Sbjct: 134 DHRVPRIYVPLKDCPDQFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEP 193

Query: 330 ETEGILTEYGVDSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLD 389  
 ETEGILTEYGVDSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLD  
 Sbjct: 194 ETEGILTEYGVDSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLD 253

Query: 390 DALACRRLTDGTFEYGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEE 449  
 DALACRRLTDGTFEYGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEE  
 Sbjct: 254 DALACRRLTDGTFEYGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEE 313

Query: 450 LCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRISCTKLSYDHAQSMIENXXXXXXXXX 509  
 LCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRISCTKLSYDHAQSMIEN  
 Sbjct: 314 LCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRISCTKLSYDHAQSMIENPTEKIPPEE 373

Query: 510 XXXXXXXXHSVEEVHQAVLNLHSIAQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCH 569  
 HSVEEVHQAVLNLHSIAQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCH  
 Sbjct: 374 ELPPISPESHSVEEVHQAVLNLHSIAQLRRQRFDGALRLDQLKLAFTLDHETGLPQGCH 433

Query: 570 IYFYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPTKMLSDLVEFCDQMGLP 629  
 IYFYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPTKMLSDLVEFCDQMGLP  
 Sbjct: 434 IYFYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPTKMLSDLVEFCDQMGLP 493

Query: 630 MDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYAL 689  
 MDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYAL  
 Sbjct: 494 MDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYAL 553

Query: 690 NVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCND 739  
 NVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCND  
 Sbjct: 554 NVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCND 603

>gi|23271317|gb|AAH36113.1| Unknown (protein for MGC:33943) [Homo sapiens]  
 Length = 612

Score = 916 bits (2368), Expect = 0.0  
 Identities = 451/532 (84%), Positives = 476/532 (89%), Gaps = 2/532 (0%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNG 108  
 IFETYMSKEDVSEGLKRGTLIQGLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNG

Sbjct: 42 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNG 101

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWS-GPDVIEA 167  
DLVVVKLLPE+ WK VKPESNDKE EA YE+DIPEE CGHH QQS K ++ PDVI+EA

Sbjct: 102 DLVVVKLLPEEHKVVVKPESNDKETEAAYESDIPEELCGHHPLQQSLKSYNDSPDVIVEA 161

Query: 168 QFDDSDSEDRHGNTSG-LVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKS 226  
QFD SSED HG T LVDGVKKLS+ ++G+ED PV KDE T I QDTR LSEKS

Sbjct: 162 QFDGSDSEDGHGITQNVLVLDGVKKLSVCVSEKGREDDAPVTKDETTTCISQDTRALSEKS 221

Query: 227 LQSAKVVYILEKKHSRAATGILKLLADKNSDLFKKALFSPSDHRVPRIYVPLKDCPD 286  
LQ+SAKVVYILEKKHSRAATG LKLLADKNS+LF+KALFSPSDHRVPRIYVPLKDCPD

Sbjct: 222 LQSAKVVYILEKKHSRAATGFLKLLADKNSLFRKALFSPSDHRVPRIYVPLKDCPD 281

Query: 287 FMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFS 346  
F+ RPKD+ANTLFICRI+DWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFS

Sbjct: 282 FVARPKDYANTLFICRIVDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFS 341

Query: 347 SEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEYGV 406  
SEVLECLPQ LPWTIPP+E KRRDLRKDCIFTIDPSTARDLDDAL+C+ L DG F+VGV

Sbjct: 342 SEVLECLPQGLPWTIPPEEFSKRRDLRKDCIFTIDPSTARDLDDALSCKPLADGNFKVGV 401

Query: 407 HIADVSFYFVEGSSLDKVAERATSVYLVQKVPMLPRLCEELCSLNPMTDKLTFSVIW 466  
HIADVSFYFVEGS LDKVAERATSVYLVQKVPMLPRLCEELCSLNPM+DKLTFSVIW

Sbjct: 402 HIADVSFYFVEGSDLDKVAERATSVYLVQKVPMLPRLCEELCSLNPMSDKLTFSVIW 461

Query: 467 KLTPEGKILEEWFGRITIRISCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXSVVEVHQA 526  
LTPEGKIL+EWFGRTIIRISCTKLSY+HAQSMIE+ HS EEVHQA

Sbjct: 462 TLTPEGKILDEWFGRTIIRISCTKLSYHAQSMIESPTEKIPAKELPPISPEHSSEEVHQA 521

Query: 527 VLNHLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNK 578  
VLNLH IAKQLR+QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYR+SNK

Sbjct: 522 VLNHLHGIKQLRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRESNK 573

>gi|21753324|dbj|BAC04324.1| unnamed protein product [Homo sapiens]  
Length = 603

Score = 812 bits (2098), Expect = 0.0  
Identities = 410/527 (77%), Positives = 436/527 (82%), Gaps = 2/527 (0%)

Query: 1 MNHPDYKLNLRXXIFETYMSKEDVS 60  
M+HPDY++NLR D IFETYMSKEDVS

Sbjct: 1 MSHPDYRMNLRPLGTGRVSAVAGPHDIGASPGDKKSKNRSTRGKKKSIFETYMSKEDVS 60

Query: 61 EGLKRGTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120  
EGLKRGTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDLVVVKLLPE+

Sbjct: 61 EGLKRGTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDLVVVKLLPEEH 120

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWS-GPDVIEAQFDDSDSEDRHG 179  
WK VKPESNDKE EA YE+DIPEE CGHH QQS K ++ PDVI+EAQFD SSED HG

Sbjct: 121 WKVVVKPESNDKETEAAYESDIPEELCGHHPLQQSLKSYNDSPDVIVEAQFDGSDSEDGHG 180

Query: 180 NTSG-LVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQSAKVVYILE 238  
T LVDGVKKLS+ ++G+ED PV KDE T I QDTR LSEKSLQ+SAKVVYILE

Sbjct: 181 ITQNVLVLDGVKKLSVCVSEKGREDDAPVTKDETTTCISQDTRALSEKSLQSAKVVYILE 240

Query: 239 KKHSRAATGILKLLADKNSDLFKKALFSPSDHRVPRIYVPLKDCPDQFMTRPKDFANTL 298  
KKHSRAATG LKLLADKNS+LF+KALFSPSDHRVPRIYVPLKDCPDQF+ RPKD+ANTL

Sbjct: 241 KKHSRAATGFLKLLADKNSLFRKALFSPSDHRVPRIYVPLKDCPDQFVARPKDYANTL 300

Query: 299 FICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLP 358  
FICRI+DWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQ LP

Sbjct: 301 FICRIVDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQGLP 360

Query: 359 WTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEYGVHIAADVSFYFVEG 418

WTIPP+E KRRDLRKDCIFTIDPSTARDLDDAL+C+ L DG F+VGVHIADVSYFVPEG  
Sbjct: 361 WTIPPEEFSKRRDLRKDCIFTIDPSTARDLDDALSCKPLADGNFKVGVHIADVSYFVPEG 420

Query: 419 SSLDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPPEGKILEEW 478  
S LDKVAAERATSVYLVQKVVPMLPRLLCEELCSLNPM+DKLTFSVIW LTPEGKIL+EW  
Sbjct: 421 SLDKVAERATSVYLVQKVVPMLPRLLCEELCSLNPM+DKLTFSVIWLTPEGKILDEW 480

Query: 479 FGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQ 525  
FGRTIIRSCTKLSY+HAQSMIE+ HS EEVHQ  
Sbjct: 481 FGRTIIRSCTKLSYDHAQSMIESPTEKIPAKELPPISPEHSSEEVHQ 527

>gi|21292324|gb|EAA04469.1| agCP3212 [Anopheles gambiae str. PEST]  
Length = 794

Score = 424 bits (1089), Expect = e-117  
Identities = 249/672 (37%), Positives = 379/672 (56%), Gaps = 35/672 (5%)

Query: 196 PDRGKEDSSTPVMKDENTPIPDQD--TRGLSEKSLQKSAAK-VVYILEKKHSRAATGILKLL 252  
P +DS+T + N ++ T+ KS Q S VV ILEK+H+R G K L  
Sbjct: 127 PKAPSDSATSPPNANGNDESABEDATQQAGGKSTQNSVGFVVAILEKRHNRCQCVG--KFL 184

Query: 253 ADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFM-----TRP 291  
A K Y +F P D R+P + V +D P + T  
Sbjct: 185 AAPGK--KHYRVFMPRDMRIPPVRVFKQDWPNNALLSTNIAKLKDDKEEKEDRKVPQTGD 242

Query: 292 KDFANTLFCRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLE 351  
D + L+ II+W+++ +G + KS+G+ G +E E IL E+ +D + + +L  
Sbjct: 243 VDVTDVLYQAEIIIEWQDEV--PIGTILKSIGKCGVLEVENESILVEHNLDVTPYGEAILA 300

Query: 352 CLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEFGVHIADV 411  
LP ++P+ IP +E+ +R DLR +CIFTIDP+TARDLDDAL+C++L +G +++GVHI+DV  
Sbjct: 301 QLP-APYQIPQEELEEREDLRGECIFTIDPATARDLDDALSCKQLENGNYQIGVHISDV 359

Query: 412 SYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTP 471  
+YF+ E S LD++ RATS+Y+V V MLP+ LC CSL P DKL FSV W++ P+  
Sbjct: 360 TYFLRESSPLDELVKLRATSIYMVDTVYHMLPKQLCNT-CSLLPGEDKLAFSVFVWEMQPD 418

Query: 472 GKILEEWFGRRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNH 531  
G +L F RT+I SC++LSY+HAQ M++N ++ +++ + V L  
Sbjct: 419 GTVLSTRFARTVINSCSQLSYEHAQMLDNPSCEVEEDQFPEIMHGYNALQCKIVNTLQ 478

Query: 532 SIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAV 591  
SIA QLR++R DG L+++Q KL F LD TG P +Y+ R SN+++E+FMMLAN +V  
Sbjct: 479 SIAVQLRQRRMDDGCLKINQPKLTFRLDPATGRPIEYGVYKVRPSNEMIEDFMMLANTSV 538

Query: 592 AHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSILTTFGDDKY 651  
A+ I++ FPE +LLR H PP M+ +LV G + +S + + + +  
Sbjct: 539 ANAIYKAFPEISLLRAHSPPAENMMKNLVRTLSLHGHALSYASPKDIRECMETIITSEN 598

Query: 652 SLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHR 711  
A + VL+ + ++PM A Y+CS E F HYAL +P+YTHFTSPIRR+AD +VHR  
Sbjct: 599 PDATRSVLSVLLAKPMIRAQYYCSLYATTPEHFHMYALAIPMYTHFTSPIRRYADCLVHR 658

Query: 712 LLAAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAM 771  
+LAAAL QP P+ LQ A CN+++ +K E S L+F ++ G E+EA  
Sbjct: 659 VLAAALAIQVQPKRSPEELQCLAMICNEKKYNAKACAGEASSLLYFRHWLEAVGEYETEAA 718

Query: 772 VMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQV 831  
VMG +++++ G+ + L+ + K +P + + P+D P +  
Sbjct: 719 VMGYAAHHIELVLIHSGIVLKAATKKLSTVATVVYK-PTEPVASCMLIPNDTSIPPVE-- 775

Query: 832 ITIFSLVDVVLQ 843  
+TIF+ V V ++  
Sbjct: 776 LTIFTKVRVTVK 787

>gi|19115422|ref|NP\_594510.1| ribonuclease II RNB family protein; dis3-like  
 [Schizosaccharomyces  
   pombe]  
 gi|7493295|pir|T38518 ribonuclease II RNB family protein - fission yeast  
   (Schizosaccharomyces pombe)  
 gi|2414618|emb|CAB16367.1| ribonuclease II RNB family protein; dis3-like  
 [Schizosaccharomyces  
   pombe]  
 Length = 927

Score = 418 bits (1075), Expect = e-115  
 Identities = 273/764 (35%), Positives = 392/764 (51%), Gaps = 91/764 (11%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDGRDIFIDGVVARNRALNG 108  
 ++ Y V +GLK GTL +G LRI H + + D ++DG +ARNRA +  
 Sbjct: 175 VYPLYDSATVKKGLKSGTLFKGTLRILEN--HRSAFACMEDIPDFYVDGPIARNRAFHN 232

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSPDVIIEAQ 168  
 D+V+V E D P E LQ + + +  
 Sbjct: 233 DVVIV-----EPVMNNDSPTEKSNF--LQNG-----VEKVK 261

Query: 169 FDDSDSEDRHGNTSGLVDGVKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQ 228  
 D D E G ++ +++L I + K DS T  
 Sbjct: 262 IKDHDDE----LGGAMEHLERLEIKSVASFKGDSRT----- 293

Query: 229 KSAKVYVILEKKHSRAATGILKL--LADKNSDLFKK--YALFSPSDHRVPRIYVPLKDC 283  
 A+VV I ++ GIL+ + KN + K YA+F P D R+P I + D  
 Sbjct: 294 -RARVVAIEKRAEISKIVGILRAPGWSLKNVEYVSKSSYAIFIPKDKRLPFITIHKNDL 352

Query: 284 P----QDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYG 339  
 ++++ + LF I W + +G L + LG ++E T +L E G  
 Sbjct: 353 SDLSGENWIENILKHDQLFSVEITRWSIYSRYPMGVLGKLGNIITDVEAYTNALLLENG 412

Query: 340 VDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRRLTD 399  
 + S FS EVL CLP W I +E+ KRRDLR + I TIDP TARDLDDA++CR L +  
 Sbjct: 413 ISSSPFSDEVLNCLPPD-DWIISHEEIKRRDLRNELIITIDPETARDLDDAVSCRALDN 471

Query: 400 GTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDK 459  
 GT+EVGVHIADV++FV S+LDK AA RAT+VYLVQK +PMLP LLCE LCSLNP ++  
 Sbjct: 472 GTYEVGVHIADVTHFVKPDSALDKAASRATTVYLVQKAIPMLPPLLCERLCSLNPNVER 531

Query: 460 LTFSVIWKLTPEGK-ILEEWFGRTIIRCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXX 518  
 L FSV WKL GK I + WFG+T+I++C +L+Y AQ +IE H  
 Sbjct: 532 LAFSVFWKLDSNGKEIGKRWFGKTVIKTCARLAYSEAQGVIEG--KSWDDAVGKPIGGTH 589

Query: 519 SVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNK 578  
 + ++V ++L L I+++LR+ RF GA+ ++ +L F LD E G+P C +YE D+N  
 Sbjct: 590 TPKDVETSILTCEISRKLKRDFAKGAVEINSTELKFQLD-EYGMPNKCEVYEQT DANH 648

Query: 579 LVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLS DLVEFCDQMGLPMDVSSAGAL 638  
 L+EEFMLLAN +VA I + F +LLRRH P+ K +++ F M D SS+ A  
 Sbjct: 649 LIEEFMLLANRSVAEHISKNFNSNLSLLRRHASPKEKQINEFCHFLKSMNFD FDASSSAF 708

Query: 639 NKSLTK---TFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYT 695  
 N S+ + TF ++ E+ NM R + A YFC+G ++ + HYAL+ YT  
 Sbjct: 709 NASMVRLRSTFNEELV----ELFENMAVRSLNRAEYFCTGDFGEKTDWHHYALSFNHYT 763

Query: 696 HFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSGLF 755  
 HFTSPIRR+ D+IVHRL +L + P ++ A HCN+++ S VQE S LF  
 Sbjct: 764 HFTSPIRRYPDIIVHRLRLERSLK-NTSPGIDKKNCSLVAHCNEKKEKSTTVQEDSQQLF 822

Query: 756 FAVLVKE-----SGPLESEAMVMGVNLQAFDVLVLRFGVQKRI 793  
 +V + E + +A + + DV + +G+ R+  
 Sbjct: 823 LSVYIAEYCKKHKDKKSMVPVQAFATRISGNSIDVYISEYGISNRV 866

>gi|15220899|ref|NP\_177891.1| putative 3'-5' exoribonuclease; protein id:  
Atlg77680.1

[Arabidopsis thaliana]  
length = 1055

Score = 414 bits (1063), Expect = e-114  
Identities = 277/810 (34%), Positives = 415/810 (51%), Gaps = 78/810 (9%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGLRINPKKFHEAFIPSPDGDRIIDFIDGVVARNRALNG 108  
IF ++ S + V+E L++G + + R+N +EA+ DI I+G V ++RA+ G  
Sbjct: 147 IFSSHWSLDAVTEALEKGEAFKALFRVNAHNRNEAYCKIDGVPTDILINGNVCSRAVEG 206

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQ 168  
D VV+KL P W +K E+ EG P + +K + +  
Sbjct: 207 DTVVIKLDPLSLWPKMK-----GFTVESAAKPEGTNSPPEKDDKKARQKNGIDVVEG 258

Query: 169 FDDSDSEDRHGNTSGLVDGVKK-LSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSL 227  
F+D S+++ +S + G K ++ S+P + + N G+  
Sbjct: 259 FEDGFSKNK---SSVIGKGAKNGVTPSSPPSLDSCLSGFCQKGNCSAVDKLCGILSSFP 315

Query: 228 QK--SAKVVIILEKKHSR-AATGILKL---LADKNSDLFK-----KYALFSPSDH 271  
K + +VV ++EK R + G+L + + K SD + +Y P+D  
Sbjct: 316 HKRPTGQVVAVVEKSLVRDSIVGLLDVKGWIHYKESDPKRCKSPLSLSDDEYVQLMPADP 375

Query: 272 RVPRIYVPLKDCPQDFMTRPK---DFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI 327  
R P++ VP P R + + L +I+DW E F + Q+ G+ E+  
Sbjct: 376 RFPKLIVPFHVLPGSIRARLENLDPNLEAELVAAQIVDWGEGSPFPVAQITHLFRGSEL 435

Query: 328 EPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD 387  
EP+ IL + V SDFS L LP+ +PW +P +EV +R+DLR C+ TIDPSTA D  
Sbjct: 436 EPQINAILYQNSVCDSDFSFGSLTSLPR-VPWEVPEEEVQRRKDLRLDLCVLTIDPSTATD 494

Query: 388 LDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLC 447  
LDDAL+ + L G F VGVHIADVSYFV ++LD A R+TSVYL+Q+ + MLP LL  
Sbjct: 495 LDDALSVQSLPGGFRRVGVHIADVSYFVLPETALDTEARFRSTSVYLMQRKISMPLPLLS 554

Query: 448 EELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRTIIRSC TKLSYDHAQSMIENXXXXXX 507  
E + SL+P D+L FS++W L EG +++ W GRTIIRSC KLSYDHAQ +I+  
Sbjct: 555 ENVGSLSPGADRLAFSILWDLNREGDVIDRWIGRTIIRSCCKLSYDHAQDIIDGKSDVAE 614

Query: 508 XXXXXXXXXXXXSVVEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQG 567  
+V ++V L I+ LR++RF +GAL+L+ K F D E G+P  
Sbjct: 615 NGWPALHGSFKWC-DVTRSVKQLSEISTTLRQKRFRNGALQLENSKPVFLFD-EHGVVPYD 672

Query: 568 CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPTKMLS DLVEFCDQMG 627  
+ SN LVEEFMLLANM A I + + +LLRRHP P T+ L + FC + G  
Sbjct: 673 FVTCSRKGSNFLVEEFMLLANMTAAEVISQAYRASSLLRRHPEPNTRKLKEFEGFCSKHG 732

Query: 628 LPMDVSSAGALNKS LTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQ-EQFRH 686  
+ +D+SS+G L SL K G+ K ++L N +PMQ+A YFC+G L+D ++ H  
Sbjct: 733 MDLDISSGQLQDSLEKITGNLKDSDSVFVDILNYYAIKPMQLASYFCTGNLKDSVAEWGH 792

Query: 687 YALNVPLYTHFTSPIRRFADVIVHR----LLAAALGYSEQPDVEPD----- 728  
YAL VPLYTHFTSP+RR+ D++VHR L A YS+Q D  
Sbjct: 793 YALAVPLYTHFTSPLRRYPDIVVHRAALAALEAEELYSKQKQTAIDEGRSCTGIHFNKD 852

Query: 729 -----TLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESG 764  
L A +CN+R++A+++V++ L+ ++K+  
Sbjct: 853 AAESIEGKEALSVAALKHGV PSTEILSDVAAYCNERKLAARKVRDACDKLYTW FVLKQKE 912

Query: 765 PLESEAMVMGVLNQAFDVLVLRFGVQKRIY 794  
EA VM + ++ V + + G+++RIY  
Sbjct: 913 IFPCEARVMNLGSRFMTVYISKLGIERRIY 942



>gi|25406521|pir||E96806 hypothetical protein T32E8.1 [imported] -  
Arabidopsis thaliana  
gi|12323300|gb|AAG51632.1|AC012193\_14 putative 3'-5' exoribonuclease, 3'  
partial; 3320-1 [Arabidopsis  
thaliana]  
Length = 935

Score = 402 bits (1033), Expect = e-110  
Identities = 274/792 (34%), Positives = 404/792 (51%), Gaps = 80/792 (10%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNG 108  
IF ++ S + V+E L++G + + R+N +EA+ DI I+G V ++RA+ G  
Sbjct: 147 IFSSHWSLDAVTEALEKGEAFKALFRVNAHRNEAYCKIDGVPTDILINGNVCSRAVEG 206

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQ 168  
D VV+KL P W +K E+ EG P + +K + +  
Sbjct: 207 DTVVVKLDPLSLWPKMK-----GFVTESAAPKPGTNSPPEKDDKKARQKNGIDVVEG 258

Query: 169 FDDSDSEDRHGNTSGLVDGVKK-LSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSL 227  
F+D S+++ +S + G K ++ S+P + + N G+  
Sbjct: 259 FEDGFSKNK---SSVIGKGAKNGVTPSSPPSLDSCLGSCFCEQKGNCSAVDKLCGILSSFP 315

Query: 228 QK--SAKVYILEKKHSR-AATGILKL---LADKNSDLFK-----KYALFSPSDH 271  
K + +VV ++EK R + G+L + + K SD + +Y P+D  
Sbjct: 316 HKRPTGQVVAVVEKSLVRDSIVGLLDVKGWIHYKESDPKRCKSPLSLSDDEYVQLMPADP 375

Query: 272 RVPRIYVPLKDCPQDFMTRPK---DFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEI 327  
R P++ VP P R + + L +I+DW E F + Q+ G+ E+  
Sbjct: 376 RFPKLIVPFHVLPGSIRARLENLDPNLEAELVAAQIVDWGEGSPFPVAQITHLFGRGSEL 435

Query: 328 EPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARD 387  
EP+ IL + V SDFS L LP+ +PW +P +EV +R+DLR C+ TIDPSTA D  
Sbjct: 436 EPQINAILYQNSVCDSDFSPLSLPR-VPWEVPVEEVQRRKDLRLDCLVLTIDPSTATD 494

Query: 388 LDDALACRLTDGTFEVGVHIADVSFYFPEGSSLDKVAERATSVYLVQKVPMPLRLLC 447  
LDDAL+ + L G F VGVHIADVSFYV ++LD A R+TSVYL+Q+ + MLP LL  
Sbjct: 495 LDDALSVQSLPGGFFRVGVHIADVSFYFVLPETALDTEARFRSTSVYLMQRKISMLPPLLS 554

Query: 448 EELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRITIRSC TKLSYDHAQSMIENXXXXXX 507  
E + SL+P D+L FS++W L EG +++ W GRTIIRSC KLSYDHAQ +I+  
Sbjct: 555 ENVGSLSPGADRLAFSILWDLNREGDVIDRWIGRTIIRSCCKLSYDHAQDIIDGKSDVAE 614

Query: 508 XXXXXXXXXXXHSEVEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQG 567  
+V ++V L I+ LR++RF +GAL+L+ K F D E G+P  
Sbjct: 615 NGWPALHGSFKWC-DVTRSVKQLSEISTTLRQKRFRNGALQLENSKPVFLEFD-EHGVYPD 672

Query: 568 CHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCDQMG 627  
+ SN LVEEFMLLANM A I + + +LLRRHP P T+ L + FC + G  
Sbjct: 673 FVTCRSRKGSNFLVEEFMLLANMTAAEVISQAYRASSLLRRHPEPNTRKLKEFEGFCSKHG 732

Query: 628 LPMDVSSAGALNKS LTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQ-EQFRH 686  
+ +D+SS+G L SL K G+ K ++L N +PMQ+A YFC+G L+D ++ H  
Sbjct: 733 MDLDISSGQLQDSLEKITGNLKDSDSVFVDILNNYAIKPMQLASYFCTGNLKDSVAEWGH 792

Query: 687 YALNVPLYTHFTSPIRRFADVIVHR----LLAALGYSEQPDVEPD----- 728  
YAL VPLYTHFTSP+RR+ D++VHR L A YS+Q D  
Sbjct: 793 YALAVPLYTHFTSPLRRYPDIVVHRALAAALEAEELYSKQKQTAIDEGRSCTGIHFNKD 852

Query: 729 -----TLQKQADHCNDRRMASKRVQELSIGLF--FAVLVKE 762  
L A +CN+R++A+++V++ L+ F+ KE  
Sbjct: 853 AAESIEGKEALSVAALKHGVPESTELSDVAAAYCNERKLAARKVRDACDKLYTWFLVKQKE 912

Query: 763 SGPLESEAMVMG 774  
P E+ M +G

Sbjct: 913 IFPCEARVMNLG 924

>gi|25332397|pir||A84553 probable mitotic control protein dis3 [imported] -  
Arabidopsis  
thaliana  
Length = 955

Score = 396 bits (1018), Expect = e-109  
Identities = 252/757 (33%), Positives = 407/757 (53%), Gaps = 84/757 (11%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNG 108  
I++ +. +++ GL RG QG LR+N +EA++ S +I I G NRA +G  
Sbjct: 215 IQEHKPMSEITAGLHRGIYHQGKLRVNRFPNPEAYVGSESIGEEIIYGRSNMRAFDG 274

Query: 109 DLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSPDVIIIEAQ 168  
D+V V+LLP DQW+ ++K + EA I S DV++  
Sbjct: 275 DIVAVELLPRDQWQ-----DEKALSIAEEAVI-----SLHDVVLNLS 311

Query: 169 F---DDSDSEDRHGNTSGL---VDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRG 221  
F +S+++D +T L VD + S + + + ++ PV  
Sbjct: 312 FFQISNSNADDEEDTVHLAPDNVDDAPRTSNLSHETSGDKNAAPV----- 357

Query: 222 LSEKSLQKSAAKVVVILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLK 281  
+ S +VV ++ +++ + G L+ ++ +ALF D R+P+I + +  
Sbjct: 358 -----RPSGRVVGVI-RRNWHSYCGSLEPMSLPAGSGGTAHALFVSKDRRIPKIRINTR 410

Query: 282 DCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGV 341  
++ + + + W + G + +G+ G+ E ETE +L E VD  
Sbjct: 411 QL-----QNLDMRIVVAVDSWDRQSRYPGSHYVRPIGKIGDKETETEVVLIENDVD 462

Query: 342 FSDFSSEVLECLPQSLPWTIPPDEVGK--RRDLRKDCIFTIDPSTARDLDDALACRRLTD 399  
+S FSS+VL CLP LPW++ ++V R+DLR +F++DP +D+DDAL C L +  
Sbjct: 463 YSPFSSQVLACLP-PLPWSVSSEDVSNPVRQDLRHLLVFSVDPPGCKDIDDALHCTSLPN 521

Query: 400 GTFEVGVHIADVSFVPEGSSSLDKVAAERATSVYLVQKVPMPLRLLCEELCSLNPMPTDK 459  
G FE+GVHIADV+ FV G+ LD A++R TSVYLV++ + MLP+ L E++CSL ++  
Sbjct: 522 GNFEELGVHIADVTFNVHPGTPLDDEASKRGTSVYLVERRIDMLPKPLTEDICSLRADVER 581

Query: 460 LTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHS 519  
L FSVIW+++P+ +I+ F ++II+S LSY AQ+ +++  
Sbjct: 582 LAFSVIWEWSPDAEIIISTRFTKSIKSSAALSYIEAQARMDDSR----- 626

Query: 520 VEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKL 579  
+ + + N++++AK +R++R GAL L ++ F +D E P +Y+ ++N++  
Sbjct: 627 TDSLTTDLRNMNTLAKIMRQRRIIDRGALTLASAEVKFDIDPENHDPLNIGMYQILEANQM 686

Query: 580 VEEFMLLANMAVAHKIFRTFPEQALLRRHPPQTKMLSDLVEFCDQMGLPMDVSSAGALN 639  
VEEFML AN++VA +I + FP +LLRRHP P +ML L+ +GL +DVSS+ AL  
Sbjct: 687 VEEFMLAANVSVAGQILKLFPSCSLLRRHPTPTREMLEPLLRTAAAIGLTLDVSSSKALA 746

Query: 640 KSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTS 699  
SL + G+D Y +++ + +R M A+YFCSG L E + HY L PLYTHFTS  
Sbjct: 747 DSLDRAVGEDPYF--NKLIRILATRCMTQAVYFCSGDLSPPE-YHHYGLAAPLYTHFTS 802

Query: 700 PIRRFADVIVHRLLAALGYSEQPDVEPD--TLQKQADHCNDRRMASKRVQELSIGLFFA 757  
PIRR+ADV VHRLLAAL+LG + P V D L AD+ N R ++ S+ L+  
Sbjct: 803 PIRRYADVIVHRLLAASLGIYKLPTVFQDRPQLTSVADNLNRYRHRNAQMAGRASVELYVL 862

Query: 758 VLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIY 794  
+ + + P + EA V+ + + F V V ++G++ +Y  
Sbjct: 863 IYFR-TRPTDEEARVVKIRSNGFIVFVPKYGIEGPVY 898

>gi|24654592|ref|NP\_728490.1| CG16940-PC [Drosophila melanogaster]  
gi|23092667|gb|AAN11425.1|AE003467\_37 CG16940-PC [Drosophila melanogaster]  
Length = 1044

Score = 367 bits (942), Expect = e-100  
Identities = 249/739 (33%), Positives = 372/739 (50%), Gaps = 82/739 (11%)

Query: 66 GTLIQGVLRINPKKFHEAFIPSPDGDRIIDFIDGV---VARNRALNGDLVVVKLL-PEDQ 120  
G +++ +R+N K +AFI + DG+ VAR A +GD V +L P Q  
Sbjct: 308 GRIVVEEIRVNRKNNRQAFIIMSTDREALERDGIIVLLPVARRYAFDGDQKVRVFLNPGAQ 367

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIIEAQFDDSDSEDRHGN 180  
+ E + EI G P G E DD++S+ +  
Sbjct: 368 GSSKTAEPSSGEIS-----GGKPSLSLADG-----EELSDDTESQGSSED 407

Query: 181 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAAVVIILEKK 240  
T +V V+ +N P A V+ I ++  
Sbjct: 408 TDNVV-----VISSDNCP-----KAFVIAITKRT 431

Query: 241 HSRAATGIL-----KLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPK-D 293  
R G + KL D+ LF K F P D RVP +YVP C + + D  
Sbjct: 432 ELRQIVGTISFTNPTKLCDDQ---LFYK---FRPYDLRVPMVYVPKDACAHHIGNKQQID 485

Query: 294 FANTLFICRIIDWKEDCN-FALGQLAKSLGQAGEIEPETEGILTEYGV-DFSDFSSEVLE 351  
+ L++ I++ DCN + +L + +G+ G ++ E + IL G+ D F ++  
Sbjct: 486 VSGLLYLAHILE--TDCNGHCIAELIQPVGRVGNLDELKAILFHNGLRDIKPFQRFID 543

Query: 352 CLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADV 411  
Q P I +++ +R+DLRK CIFTIDP TARDLDDA++ +L D +E+GVHI+DV  
Sbjct: 544 IYSQPPP-PISQEDLRQRKDLRMCIFTIDPMTARDLDDAVSIEKLGDN EY EIGVHISDV 602

Query: 412 SYFVPEGSSSLDKVAAERATSVYLQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPE 471  
S+F+ E + LD + ER+TS+YL +V+ MLP+ LC CSL P DK FSV W++ +  
Sbjct: 603 SHFLIEDNLDNIVKERSTSIYLANEVIHMLPQSLCMR-CSLLPGQDKFAFSVFWRMNGK 661

Query: 472 GKILEE--WFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLN 529  
G +L++ F RT+I SC++ +Y+HAQ +I+N + +++ VL  
Sbjct: 662 GVMLQKKPEFCRTVINSCSQFAYEHAQKIIDNPNRFTENDFPTILNGFNPDIDIRNVLW 721

Query: 530 LHSIAKQLRRQRFDVGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMILLANM 589  
LH IA +R+ R +GAL ++ KL F LD TG P + + R++N+L+EEFMILLAN  
Sbjct: 722 LHDIASSIRKTRLDNGALTINNAKLRLFLDPITGEPLSFEVEKQREANRLIEEFMILLANQ 781

Query: 590 AVAHKIFRTFPEQALLRRHPPQTKMLSDLVFCDQMGLPMDVSSAGALNKSILTKTFGDD 649  
AVA I +FP+ A+LR HPPP K L L E +G +D SS+ AL +S+ + +  
Sbjct: 782 AVARFIHDSFPDIAVLRNHPPPLIKSLKALREKLLALGFELDYSSSKALQESMVRCLNEA 841

Query: 650 KYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQRHYALNVPLYTHFTSPIRRFADVIV 709  
+A L+ + +PM A YFCS + HYAL++P+YTHFTSPIRR+ D++V  
Sbjct: 842 PNPVAMNACLSQLLMKPMARATYFCSEKSEPADLWHYALSIPIYTHFTSPIRRYPDILV 901

Query: 710 HRLAAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESE 769  
HRLAAAL Y P PD L N+R+ +K+ E S L+F V +  
Sbjct: 902 HRLAAALKYCTPPKRTPDLDLHTLTKLANERKYNKAKGAGEDSGNLYFKRYVHNKQGIYMR 961

Query: 770 AMVMGVNLQAFDVLVLRFG 788  
A+V+ + +V+ L G  
Sbjct: 962 AVVIEIFQHMMNVVTLESG 980

>gi|19922976|ref|NP\_612012.1| CG16940-PA [Drosophila melanogaster]  
gi|24654597|ref|NP\_728491.1| CG16940-PB [Drosophila melanogaster]  
gi|16198179|gb|AAL13898.1| LD37985p [Drosophila melanogaster]  
gi|23092668|gb|AAF47351.2| CG16940-PA [Drosophila melanogaster]  
gi|23092669|gb|AAN11426.1|AE003467\_39 CG16940-PB [Drosophila melanogaster]  
Length = 1032

Score = 367 bits (942), Expect = e-100  
Identities = 249/739 (33%), Positives = 372/739 (50%), Gaps = 82/739 (11%)

Query: 66 GTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGV---VARNRALNGDLVVVKLL-PEDQ 120  
 G +++ +R+N K +AFI + DG+ VAR A +GD V +L P Q  
 Sbjct: 296 GRIVEEEIRVNRKNNRQAFIIMSTDREALERDGI VLLPVARRYAFDGDKVRAFVLNPGAQ 355

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIIEAQFDDSDSEDRHGN 180  
 + E + EI G P G E DD++S+ +  
 Sbjct: 356 GSSKTAEPSSGEIS-----GGKPSLSLADG-----EELSDDTESQGSSED 395

Query: 181 TSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAAVVYILEKK 240  
 T +V V+ +N P A V+ I ++  
 Sbjct: 396 TDNVV-----VISSDNCP-----KAFVIAITKRT 419

Query: 241 HSRAATGIL-----KLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPK-D 293  
 R G + KL D+ LF K F P D RVP +YVP C + + D  
 Sbjct: 420 ELRQIVGTISFTNPTKLCDDQ---LFYK---FRPYDLRVPMVYVPKDACA AHIGNKQQID 473

Query: 294 FANTLFICRIIDWKEDCN-FALGQLAKSLGQAGEIEPETEGILTEYGV-DFSDFSSEVLE 351  
 + L++ I++ DCN + +L + +G+ G ++ E + IL G+ D F ++  
 Sbjct: 474 VSGLLYLAHILE--TDCNGHCIAELIQPVGRVGNLDELKAILFHNGLRDIKPFQRFID 531

Query: 352 CLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADV 411  
 Q P I +++ +R+DLRK CIFTIDP TARDLDDA++ +L D +E+GVHI+DV  
 Sbjct: 532 IYSQPPP-PISQEDLRQRKDLRKMCIFTIDPMTARDLDDAVSIEKLG DNEYEIGVHISDV 590

Query: 412 SYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTP 471  
 S+F+ E + LD + ER+TS+YL +V+ MLP+ LC CSL P DK FSV W++ +  
 Sbjct: 591 SHFLIEDNLDNIVKERSTSIYLANEVIHMLPQSLCMR-CSLLPGQDKFAFSVFWRMNGK 649

Query: 472 GKILEE--WFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLN 529  
 G +L++ F RT+I SC++ +Y+HAQ +I+N + +++ VL  
 Sbjct: 650 GVMLQKKPEFCRTVINSCSQFAYEHAQKI IDNPNERFTENDFPTILNGFNPDDIRNRVLW 709

Query: 530 LHSAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANM 589  
 LH IA +R+ R +GAL ++ KL F LD TG P + + R++N+L+EEFMLLAN  
 Sbjct: 710 LHDIASSIRKTRLDNGALTINNAKLRFLDPITGEPLSFEVEKQREANRLIEEFMLLANQ 769

Query: 590 AVAHKIFRTFPEQALLRRHPPPTKMLSDLVEFCQMGLPMDVSSAGALNKSLTKTFGDD 649  
 AVA I +FP+ A+LR HPPP K L L E +G +D SS+ AL +S+ + +  
 Sbjct: 770 AVARFIHDSFPDIAVLRNHPPLIKSLKALREKLLALGFELDYSSSKALQESMVRCLNEA 829

Query: 650 KYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIV 709  
 +A L+ + +PM A YFCS + HYAL++P+YTHFTSPIRR+ D++V  
 Sbjct: 830 PNPVAMNACLSQLLMKPMARATYFCSEKSEPADLWHYALSIPIYTHFTSPIRRYPDILV 889

Query: 710 HRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESE 769  
 HRLLAAL Y P PD L N+R+ +K+ E S L+F V +  
 Sbjct: 890 HRLLAALKYCTPPKRTPDLDLHTLTCLANERKYNACKAGEDSGNLYFKRYVHNKQGIYMR 949

Query: 770 AMVMGVNLQAFDVLVLRFG 788  
 A+V+ + +V+ L G  
 Sbjct: 950 AVVIEIFQHMMNVVTLESG 968

>gi|15292611|gb|AAK93574.1| SD10981p [Drosophila melanogaster]  
 Length = 982

Score = 351 bits (901), Expect = 2e-95  
 Identities = 249/815 (30%), Positives = 407/815 (49%), Gaps = 110/815 (13%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNGD 109  
 + ++S +++ EGL++ L+QG + + + + E + ++ I I G + NRA++GD  
 Sbjct: 232 YPHLSMKELLEGLRQNKLLQGTFQASRENYLEGTVNVEKFEKGILIQGRESLNRAVDGD 291

Query: 110 LVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIIIEAQF 169  
 LV V+LLPE +W A P E + Y ++P  
 Sbjct: 292 LVAVELLPEAEWSA--PSEIVLEEKVYADEVP----- 322

Query: 170 DDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQK 229  
SE+R + + +++ V+ ++S E TP  
Sbjct: 323 ----SEERAKDENEMLNQVRAAALSA-----ERTP----- 348

Query: 230 SAKVVYILEKKHSRAATGILK--LLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDF 287  
+ ++V I+ +K R GIL+ L+ D N +F P+D ++PRI + +  
Sbjct: 349 TGRIVGIVRRKW-RQYCGILQPSLIEDTNRH-----IFVPADRKIPRIRIETRQAAM-- 399

Query: 288 MTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFS 347  
N I I W + + G +SLG G++ E E IL E+ V FS  
Sbjct: 400 -----LQNQRIIVTIDTWPRNSRYPHGHFVRSLSGPLGDMATENEVILLEDHDPHCKFSD 453

Query: 348 EVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVH 407  
EVL LP+ +PWTI ++ KR DLR I ++DP D+DDAL CR L +G EVGVH  
Sbjct: 454 EVLSFLPK-MPWTITDEDYSKRVDLRDLYICSVDPGCTDIDDALHCRELPNGNLEGVH 512

Query: 408 IADVSFYFVPEGSSLDKVAERATSVYLVQKVVPMPLPRLLCEELCSLNPMTDKLTFSVIWK 467  
IADVS+F+ G++LD AA R T+VYLV K + M+P LL LCSL ++ FS +W+  
Sbjct: 513 IADVSHFIRPGNALDMEAAARGTTVYLVGKRIDMVPELLSSNLCSLVGGVERFAFSCVWE 572

Query: 468 LTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAV 527  
+ E +L + F +++I+S ++Y+ AQ++I++ E+ +++  
Sbjct: 573 VDNEANVLSKRFHKSIVIKSKRAMTYEEAQNIIDDATQQ-----NEIAKSL 617

Query: 528 LNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLA 587  
NL+ +AK L+++R +GAL L ++ F +D ET P + + R++N +VEEFMLLA  
Sbjct: 618 RNLNRLAKILKKRRMDNGALVLASPEIRFQVDSETHEPLEVEVKQMETNSMVVEEFMLLA 677

Query: 588 NMAVAHKIFRTFPEQALLRRHPPPQTKMLSDLVFCDQMGLPMDVSSAGALNKSILTKTF- 646  
N+ VA I F E A+LRRHP P LV+ G +D++S L+ SL K  
Sbjct: 678 NITVAEHIAFSECAVLRHRPRPPPTNFDPLVKSARYQGQVDINSGLLELSHSLDKCVK 737

Query: 647 GDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFAD 706  
D+ Y +LT +R M A+YF SG LQ +E+F HY L P+YTHFTSPIRR++D  
Sbjct: 738 ADNPFYNTMIRILT---TRCMMQAVYFISGSLQ-KEEFFHYGLAAPIYTHFTSPIRRYSD 793

Query: 707 VIVHRLLAALG----YSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKE 762  
++VHRLLA++G Y++ D + + ++ + N R ++ S+ L + +  
Sbjct: 794 IMVHRLLAASIGADSTYAQLLDRKSN--EELCHNLNRYRHKMAQYAGRASVALNTHLFFRG 851

Query: 763 SGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDD 822  
+ E V+ V A VL+ ++G++ +Y + ++V K E+ + +D  
Sbjct: 852 KEE-DEEGYVLFVRKNALQVLIPKYGLEGTLYLKSDDKDGKDGVERV--KSEIVFTFNEED 908

Query: 823 LEEPTQQVITIFSLVDVVLQAEATAALKYSAILKR 857  
+ V F V V L +++ +++ ++ R  
Sbjct: 909 HTQRCGDVVFHSFDPVTVRLSLDSSNVQHEKLIFR 943

>gi|18488261|ref|XP\_081229.1| Dis3 [Drosophila melanogaster]  
gi|24649634|ref|NP\_651246.2| CG6413-PA [Drosophila melanogaster]  
gi|7301148|gb|AAF56281.1| CG6413-PA [Drosophila melanogaster]  
Length = 982

Score = 350 bits (898), Expect = 6e-95  
Identities = 248/815 (30%), Positives = 407/815 (49%), Gaps = 110/815 (13%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRDIFIDGVVARNRALNGD 109  
+ ++S +++ EGL++ L+QG + + + + E + ++ I I G + NRA++GD  
Sbjct: 232 YPPHLSMKELLEGLRQNKLLQGTFOASRENYLECTVNVKEKFEKGILIQGRESLNRAVDGD 291

Query: 110 LVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSPDVIIEAQF 169  
LV V+LLPE +W A P E + Y ++P  
Sbjct: 292 LVAVELLPEAEWSA--PSEIVLEEKNVYADEVP----- 322

Query: 170 DDSSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPODTRGLSEKSLQK 229  
SE+R + + +++ V+ ++S E TP  
Sbjct: 323 ----SEERAKDENEMLNQVRAAALSA-----ERTP----- 348

Query: 230 SAKVVYILEKKHSRAATGILK--LLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDF 287  
+ ++V I+ +K R GIL+ L+ D N +F P+D ++PRI + +  
Sbjct: 349 TGRIVGIVRRKW-RQYCGILQPSLIEDTNRH-----IFVPADRKIPRIRIETROAAM-- 399

Query: 288 MTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFS 347  
N I I W + + G +SLG G++ E E IL E+ V FS  
Sbjct: 400 -----LQNQRIIVTIDTWPRNSRYPHGHFVRSLSGLPLGDMATENEVILLEDVPHCKFS 453

Query: 348 EVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEYGVH 407  
EVL LP+ +PWTI ++ KR DLR I ++DP D+DDAL C+ L +G EVGVH  
Sbjct: 454 EVLSFLPK-MPWTITDEDYSKRVDLRDLYICSVDPGCTDIDDALHCKELPNGNLEVGVH 512

Query: 408 IADVSYFVPEGSSLDKVAERATSIVLVQKVPMPLPRLLCEELCSLNPMTDKLTFSVIWK 467  
IADVS+F+ G++LD AA R T+VYLV K + M+P LL LCSL ++ FS +W+  
Sbjct: 513 IADVSHFIRPGNALDMEAAARGTTVYLVGKRIDMVPELLSSNLCSLVGGVERFAFSCVWE 572

Query: 468 LTPEGKILEEWFGRTIIRSC TKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAV 527  
+ E +L + F +++I+S ++Y+ AQ++I++ E+ +++  
Sbjct: 573 VDNEANVLSKRFBKSVIKSKRAMTYEEAQNIIDDATQQ-----NEIAKSL 617

Query: 528 LNLHSLAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYERDSNKLVEEFMLLA 587  
NL+ +AK L+++R +GAL L ++ F +D ET P + + R++N +VEEFMLLA  
Sbjct: 618 RNLNRLAKILKKRMDNGALVLASPEIRFQVDSETHEPLEVEVKQMRETNSMVEEFMLLA 677

Query: 588 NMAVAHKIFRTFPEQALLRRHPPPQTMLSDLVFECDQMGLPMDVSSAGALNKS LTKTF- 646  
N+ VA I F E A+LRRHP P LV+ G +D++S L+ SL K  
Sbjct: 678 NITVAEHIAEFSECAVLRHPRPPPTNFDPLVKSARYQGFQVDINSGLLESLDKCVK 737

Query: 647 GDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFAD 706  
D+ Y +LT +R M A+YF SG LQ +E+F HY L P+YTHFTSPIRR++D  
Sbjct: 738 ADNPFYNTMIRILT---TRCMMQAVYFISGSLQ-KEEFFHYGLAAPIYTHFTSPIRRYS 793

Query: 707 VIVHRLLAALG---YSEQPDVEPDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKE 762  
++VHRLLA++G Y++ D + + ++ + N R ++ S+ L + +  
Sbjct: 794 IMVHRLLAASIGADSTYAQLLDRKSN--EELCHNLNRYHKMAQYAGRASVALNTHLFFRG 851

Query: 763 SGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDD 822  
+ E V+ V A VL+ ++G++ +Y + ++V K E+ + +D  
Sbjct: 852 KEE-DEEGYVLFVRKNALQVLIPKYGLEGTLYLKSDDKDGKGVVERV--KSEIVFTFNEED 908

Query: 823 LEEPTQQVITIFSLVDVVLQAEATALKYSAILKR 857  
+ V F V V L +++ +++ ++ R  
Sbjct: 909 HTQRCGDVVFHSFDPVTVRLSLDSSNVQHEKLIFR 943

>gi|21748526|dbj|BAC03400.1| FLJ00327 protein [Homo sapiens]  
Length = 266

Score = 343 bits (879), Expect = 9e-93  
Identities = 167/188 (88%), Positives = 175/188 (93%)

Query: 578 KLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTMLSDLVFECDQMGLPMDVSSAGA 637  
+LVEEFMLLANMAVAHKI R FPEQALLRRHPPPQT+MLSDLVFECDQMGLP+D SSAGA  
Sbjct: 29 RLVEEFMLLANMAVAHKIHRAFPEQALLRRHPPPQTRMLSDLVFECDQMGLPVDFSSAGA 88

Query: 638 LNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHF 697  
LNKSLT+TFGDDKYSLARKEVLTNM SRPMQMALYFCSG+LQD QFRHYALNVPLYTHF  
Sbjct: 89 LNKSLTQTFGDDKYSLARKEVLTNMCSRPMQMALYFCSGLLQDPAQFRHYALNVPLYTHF 148

Query: 698 TSPIRRFAADVIVHRLLAALGYSEQPDVEPDTLQKQADHCNDRRMASKRVQELS LFFA 757  
TSPIRRFAADV+VHRLLAALGY E+ D+ PDTLQKQADHCNDRRMASKRVQELS LFFA  
Sbjct: 149 TSPIRRFAADVIVHRLLAALGYRERLDMAPDTLQKQADHCNDRRMASKRVQELSTSLFFA 208

Query: 758 VLVKESGP 765  
VLVK S P  
Sbjct: 209 VLVKVSPP 216

>gi|26327903|dbj|BAC27692.1| unnamed protein product [Mus musculus]  
Length = 687

Score = 340 bits (871), Expect = 7e-92  
Identities = 233/670 (34%), Positives = 344/670 (51%), Gaps = 60/670 (8%)

Query: 192 SISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAKVYILEKKHSRAATGILKL 251  
S+ D G+ + V KDE + T +SEK L+ + +VV I+ K++ R G+L  
Sbjct: 36 SVVLDDEGQNEED--VEKDEERELLLKT-AVSEKMLRPTGRVVGII-KRNWRPYCGMLSK 91

Query: 252 LADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCN 311  
K S + LF+P+D R+PRI + + + I I W +  
Sbjct: 92 SDIKES----RRHLFTPADKRIPRIRIETR-----QASALEGRRIIIVADGWPRNSR 139

Query: 312 FALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRD 371  
+ G K+LG GE E ETE +L E+ V FS VL LP+ +PW+I +++ R D  
Sbjct: 140 YPNGHFVKNLGADVGEKETETEVLLLEHDVPHQPFSSQAVLSFLPR-MPWSITEEDMKNRED 198

Query: 372 LRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSFYFVPEGSSLDKVAERATS 431  
LR C+ ++DP D+DDAL CR L++G EVGVHIADVS+F+ G++LD+ +A R T+  
Sbjct: 199 LRHLVCVSDPPGCTDIDDALHCRELSNGNLEVGVHIADVSHFIRPGNALDQESARRGTT 258

Query: 432 VYLQKVVPMPLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLS 491  
VYL +K + M+P LL LCSL D+L FS IW++ +IL+ F +++I S L+  
Sbjct: 259 VYLCEKRIDMVPELLSSNLCSLRSNVDRLAFSCIWEMNHNAEILKTRFTKSVINSKASLT 318

Query: 492 YDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQ 551  
Y AQ I++ +++ ++ L+ +AK L++ R GAL L  
Sbjct: 319 YAEAQMRIDSAMN-----DDITSLRGLNQLAKILKKGRIEKGALTLSS 363

Query: 552 LKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPP 611  
++ F +D ET P E R++N +VEEFMLLAN++VA KI F E ALLR+HP P  
Sbjct: 364 PEIRFHMDSETHDPIDLQTKELRETNMVEEFMLLANISVAKKIHEEFSEHALLRKHPAP 423

Query: 612 QTKMLSDLVEFCDQMGLPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLTNMYSRPMQMAL 671  
LV+ L + +A +L SL + D L +L + +R M A+  
Sbjct: 424 PPSNYDILVKAASKNLQIKTDTAKSLADSLDRAESPDPYPL--NTLLRILATRCMMQAV 481

Query: 672 YFCSGMLQDQEQRHYALNVPLYTHFTSPIRRFADVIVHRLLAALG---YSEQPDVEP 727  
YFCSGM D F HY L P+YTHFTSPIRR+AD+IVHRLLA A+G Y E D  
Sbjct: 482 YFCSGMDND---FHHYGLASPIYTHFTSPIRRYADIIVHRLLAIVAIGADCTYPELTDK-- 536

Query: 728 DTLQKQADHC---NDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLV 784  
K +D C N R ++ Q S+ + K G + EA ++ V A VL+  
Sbjct: 537 ---HKLSICKNLNFRHKMAQYASQASVAFHTQLFFKSKGIVSEEAYILFVRKNAIVVLI 593

Query: 785 LRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQA 844  
++G++ ++ +K KP L E L E T V +F V V +  
Sbjct: 594 PKYGLEGTVFVE-----EKDKPKPRLAYDDEIPSLRIEKT--VFHVFDKVKVKITL 642

Query: 845 EATALKYSAI 854  
+++ L++ I  
Sbjct: 643 DSSNLQHQKI 652

Score = 37.7 bits (86), Expect = 0.87  
Identities = 20/54 (37%), Positives = 32/54 (59%), Gaps = 2/54 (3%)

Query: 91 DRDIFIDGVVARNRALNGDLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEE 144  
+++I I G+ NRA++ D+V V+LLP QW V P S + E E D+ ++

Sbjct: 1 EKEILIQGIKHLNRAVHEDIVAVELLPRSQW--VAPSSVVLDDDEGQNEDDVEKD 52

>gi|13446610|emb|CAC35051.1| putative exoribonuclease DIS3 [Drosophila melanogaster]

Length = 983

Score = 335 bits (859), Expect = 2e-90

Identities = 244/816 (29%), Positives = 401/816 (49%), Gaps = 111/816 (13%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGDRIIDFIDGVVARNRALNGD 109  
+ ++S +++ EGL++ L+QG + + + + E + ++ I I G + NRA++GD

Sbjct: 232 YPHLSMKELLEGLRQNKLLQGTTFQASRENYLEGTVNVEKFEKGILIQGRESLNRAVDGD 291

Query: 110 LVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVIEAQF 169  
LV V+LLPE +W A P E + Y ++P

Sbjct: 292 LVAVELLPEAEWSA--PSEIVLEEKNVYADEVP----- 322

Query: 170 DDSSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSSTPVMKDENTPIPDTRGLSEKSLQK 229  
SE+R + + +++ V+ ++S E TP

Sbjct: 323 ----SEERAKDENEMLNQVRAAALSA-----ERTP----- 348

Query: 230 SAKVVYILEKKHSRAATGILK--LLADKNSDLFKKYALFSPSDHRVPRIYVPLKDQCPQDF 287  
+ ++V I+ +K R GIL+ L+ D N +F P+D ++PRI + +

Sbjct: 349 TGRIVGIVRRKW-RQYCGILQPSLIETNRH-----IFVPADRKIPRIRIETRQAAM-- 399

Query: 288 MTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSS 347  
N I I W + + G +SLG G++ E E IL E+ V FS

Sbjct: 400 -----LQNQRIIVTIDTWPRNSRYPHGHFVRSLSGLPLGDMATENEVILLEHDVPHCKFSD 453

Query: 348 EVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVH 407  
EVL LP+ +PWTI ++ KR DLR I ++DP D+DDAL CR L +G EVGVH

Sbjct: 454 EVLSFLPK-MPWTITDEDYSKRVDLRDLYICSDVPPGCTDIDDALHCRELPNGNLEVGVH 512

Query: 408 IADVSFYFVEGSSLDKVAERA-TSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIW 466  
IADVS+F+ G + T+VYLV K + M+P LL LCSL ++ FS +W

Sbjct: 513 IADVSHFIRPGKRTGHGGSGPGETTVYLVGKRIDMVPELLSSNLCSLVGGVERFAFSCVW 572

Query: 467 KLTPEGKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQA 526  
++ E +L + F +++I+S ++Y+ AQ++I++ E+ ++

Sbjct: 573 EVDNEANVLSKRFHKSVIKSKRAMTYEEAQNIIDDATQQ-----NEIAKS 617

Query: 527 VLNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMML 586  
+ NL+ +AK L+++R +GAL L ++ F +D ET P + + R++N +VEEFMML

Sbjct: 618 LRNLNRLAKILKRRMDNGALVLASPEIRFQVDSETHEPLEVEVKQMRETNSMVEEFMML 677

Query: 587 ANMAVAHKIFRTFPEQALLRRHPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSILTKTF 646  
AN+ VA I F E A+LRRHP P LV+ G +D++S L+ SL K

Sbjct: 678 ANITVAEHIAFSECAVLRHRHPRPPTNFDPLVKSARYQGFQVDINSGLELSHSLDKCV 737

Query: 647 -GDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQRHYALNVPLYTHFTSPIRRFA 705  
D+ Y +LT +R M A+YF SG LQ +E+F HY L P+YTHFTSPIRR++

Sbjct: 738 KADNPYFNTMIRILT---TRCMMQAVYFISGSLQ-KEEFFHYGLAAPIYTHFTSPIRRYS 793

Query: 706 DVIVHRLLAALG---YSEQPDVEPDTLQKQADHCNDRMASKRVQELSIGLFFAVLVK 761  
D++VHRLLA++G Y++ D + + ++ + N R ++ S+ L + +

Sbjct: 794 DIMVHRLLAASIGADSTYAQLLDRKSN--EELCHNLNRYHKMAQYAGRASVALNTHLFFR 851

Query: 762 ESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPD 821  
+ E V+ V A VL+ ++G++ +Y + ++V K E+ + +

Sbjct: 852 GKEE-DEEGYVLFVRKNALQVLIPKYGLEGTLYLKSDKDGKDGVERV--KSEIVFTFNEE 908

Query: 822 DLEEEPTQQVITIFSLVDVVLQAEATALKYSAILKR 857  
D + V F V V L +++ +++ ++ R

Sbjct: 909 DHTQRCGDVVFHSFDPVTVRLSLDSSNVQHEKLIFR 944



>gi|5262619|emb|CAB45749.1| hypothetical protein [Homo sapiens]  
Length = 632

Score = 334 bits (856), Expect = 4e-90  
Identities = 226/644 (35%), Positives = 335/644 (52%), Gaps = 65/644 (10%)

Query: 222 LSEKSLQKSAKVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLK 281  
+SEK L+ + +VV I+ K++ R G+L K S + LF+P+D R+PRI + +  
Sbjct: 8 VSEKMLKPTGRVVGII-KRNWRPYCGMLSKSDIKES----RRHLFTPADKRIPRIRIETR 62

Query: 282 DCPQDFMTRPKDFANTLFICRII---DWKEDCNFALGQLAKSLGQAGEIEPETEGILTE 337  
A+TL RII W + + G ++LG GE E ETE +L E  
Sbjct: 63 Q-----ASTLEGRRIIIVADGWPRNSRYPNGHFVRNLGDVGEKETETEVLLLE 110

Query: 338 YGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRL 397  
+ V FS VL LP+ +PW+I ++ R DLR CI ++DP D+DDAL CR L  
Sbjct: 111 HDVPHQPFSSQAVLSFLPK-MPWSITEKDMKNREDLRHLCCSVDPPGCTDIDDALHCREL 169

Query: 398 TDGTFEVGVIADVSFYVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEELCSLNPM 457  
+G EVGVHIADVS+F+ G++LD+ +A R T+VYL +K + M+P LL LCSL  
Sbjct: 170 ENGNLEVGVIADVSHFIRPGNALDQESARRGTTVYLCERIDMVPELLSSNLCSLKCDV 229

Query: 458 DKLTFSVIWKLTPGKILEEWFGRITII RSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXX 517  
D+L FS IW++ +IL+ F +++I S L+Y AQ I++  
Sbjct: 230 DRLAFSCIWEMNHNAEILKTKFTKSVINSKASLTAEALRIDSANMN----- 277

Query: 518 HSEVEVHQAVLNLHSLAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSN 577  
+++ ++ L+ +AK L+++R GAL L ++ F +D ET P E R++N  
Sbjct: 278 ---DDITTSRLGLNKLAKILKKRIEKGALTSSPEVRFHMDSETHDPIDLTQKELRET 334

Query: 578 KLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPTKMLSDLVEFCDQMGLPMDVSSAGA 637  
+VEEFMLLAN++VA KI F E ALLR+HP P LV+ L + +A +  
Sbjct: 335 SMVEEFMLLANISVAKKIHSEHFSEHALLRKHPAPPPSNYEILVKAARSRLNLEIKTDTAKS 394

Query: 638 LNKSLTKTFGDDKYSLARKEVLNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPYLYTHF 697  
L +SL + L +L + +R M A+YFCSGM D F HY L P+YTHF  
Sbjct: 395 LAESLDQAESPTFPYL--NTLLRILATRCMMQAVYFCSGMDND---FHHYGLASPIYTHF 449

Query: 698 TSPIRRFADVIVHRLLAALG----YSEQPDVEPDTLQKQADHC---NDRRMASKRVQEL 750  
TSPIRR+ADVIVHRLLA A+G Y E D K AD C N R ++ Q  
Sbjct: 450 TSPIRRYADVIVHRLLAIVAIGADCTYPELTDK-----HKLADICKNLNFRHKMAQYAQRA 504

Query: 751 SIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGK 810  
S+ + K G + EA ++ V A VL+ ++G++ + F +  
Sbjct: 505 SVAFHTQLFPKSKGIVSEEAYILFVRKNAIVVLIPKYGLEGTV-----FFEEKD 553

Query: 811 KP ELTLVWEPDDLEEEPTQQVITIFSLVDVVLQAEATALKYSAI 854  
KP L+++ + + V +F V V + +++ L++ I  
Sbjct: 554 KPNPQLIYDDEIPSLKIEDTVFHVFDKVKVKIMLDSSNLQHQKI 597

>gi|27703387|ref|XP\_224449.1| similar to mitotic control protein dis3  
homolog [Homo sapiens]  
[Rattus norvegicus]  
Length = 1034

Score = 330 bits (846), Expect = 7e-89  
Identities = 233/679 (34%), Positives = 343/679 (50%), Gaps = 69/679 (10%)

Query: 192 SISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQKSAKVYILEKKHSRAATGILKL 251  
S+ D G+ + V KDE + T +SEK L+ + +VV I+ K++ R G+L  
Sbjct: 374 SVVLHDEGQNEDD--VEKDEERELLLKT-AVSEKMLRPTGRVVGII-KRNWRPYCGMLSK 429

Query: 252 LADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCN 311  
K S + LF+P+D R+PRI + + + I I W +  
Sbjct: 430 SDIKES----RRHLFTPADKRIPRIRIETR-----QASALEGRRIIVADGWPRNSR 477

Query: 312 FALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRD 371  
 + G K+LG GE E ETE +L E+ V FS VL LP+ +PW+I +++ R D  
 Sbjct: 478 YPNGHFVKNLGDVGEKETETEVLLLEHDVPHQPFSSQAVLSFLPK-MPWSITEEDMKNRD 536

Query: 372 LRKDCIFTIDPSTARDLDDALACRRLTDGTFEYGVHIAVSYFVPEGSSLDKVAERATS 431  
 LR C+ ++DP D+DDAL CR L++G EVGVHIAVDS+F+ G++LD+ +A R T+  
 Sbjct: 537 LRHLVCVSDPPGCTDIDDALHCRELSNGNLEVGVHIAVDSHFIRPGNALDQESARRGTT 596

Query: 432 VYLVQKVVPMLPRLLCEELCSLNPMTDKL-----TFSVIWKLTPEGKILEEWFGR 482  
 VYL +K + M+P LL LCSL D+ F IW++ +IL+ F ++  
 Sbjct: 597 VYLCEKRIDMVPELLSSNLCSLRSNVDRYFCIVFDKXWHFPXIWEMNHNAEILKTRFTKS 656

Query: 483 IIRSTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRRQRF 542  
 +I S L+Y AQ I++ +++ ++ L+ +AK L+R R  
 Sbjct: 657 VINSKASLTIAEAQMRIDSAAMN-----DDITSLRGLNKLAKILKRGRI 701

Query: 543 VDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQ 602  
 GAL L ++ F +D ET P E R++N +VEEFMLLAN++VA KI F E  
 Sbjct: 702 EKGALTLSSPEIRFHMDSETHDPIDLQTKELRETNMVEEFMLLANISVAKKIH EEFSEH 761

Query: 603 ALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTMN 662  
 ALLR+HP P LV+ L + +A +L SL + D L +L +  
 Sbjct: 762 ALLRKHPAPPPSNYEVLVKAASKNLEIRTD TAKSLADSLDRAECPDFPYL--NTLLRIL 819

Query: 663 YSRPMQMALYFCSGMLQDQEQRHYALNVPLYTHFTSPIRRFADVIVHRLLAALG---- 718  
 +R M A+YFCSGM D F HY L P+YTHFTSPIRR+AD+IVHRLLA A+G  
 Sbjct: 820 ATRCMMQAVYFCSGMDS---FHHYGLASPIYTHFTSPIRRYADIIVHRLLAIVAIGADCT 876

Query: 719 YSEQPDVEPDTLQKQADHC---NDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGV 775  
 Y E D K +D C N R ++ Q S+ + K G + EA ++ V  
 Sbjct: 877 YPELTDK-----HKLS DICKNLNFRHKMAQYAQRASVAFHTQLFFKSKGIVSEAYILFV 931

Query: 776 LNQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIF 835  
 A VL+ ++G++ ++ +K KP LT E L E T V +F  
 Sbjct: 932 RKNIAIVVLIPKYGLEGTVFEE-----EKDKPKPRLTYDDEIPSLRIEGT--VFHVF 980

Query: 836 SLVDVVLQAEATALKYSAI 854  
 V V + +++ L++ I  
 Sbjct: 981 DKVKVKITLDSSNLQHQKI 999

Score = 51.6 bits (122), Expect = 5e-05  
 Identities = 30/99 (30%), Positives = 54/99 (54%), Gaps = 5/99 (5%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGLVLRINPKKFHEAFI---PSPDGDRIIDIFIDGVVARNRA 105  
 IF ++ +G+K G+ +QG R + + + EA + + +++I I G+ NRA  
 Sbjct: 294 IFSEHLPLSKLQQGIKSGSYLQGTFRASRENYLEATVWIHGDKEDKEKEILIQGLKHLNRA 353

Query: 106 LNGDLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEE 144  
 ++ D+V V+LLP+ QW V P S E E D+ ++  
 Sbjct: 354 IHEDIVAVELLPKSQW--VAPSSVVLHDEGQNEDDVEKD 390

>gi|19923416|ref|NP\_055768.2| mitotic control protein dis3 homolog [Homo sapiens]  
 gi|17225572|gb|AAL37479.1|AF330044\_1 KIAA1008 protein [Homo sapiens]  
 Length = 958

Score = 330 bits (845), Expect = 7e-89  
 Identities = 229/674 (33%), Positives = 344/674 (51%), Gaps = 68/674 (10%)

Query: 192 SISTPDRGKEDSSTPVMKIDENTPIPDTRGLSEKSLQKSAKVYILEKKHSRAATGILKL 251  
 S+ D G+ + ++ + +SEK L+ + +VV +I+ K++ R G+L  
 Sbjct: 307 SVVLHDEGQNEEDVEKEEETERMLKT--AVSEKMLKPTGRVVGII-KRNWRPYCGMLSK 362

Query: 252 LADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRII----DWK 307  
K S + LF+P+D R+PRI + + A+TL RII W  
Sbjct: 363 SDIKES----RRHLFTPADKRIPRIETRO-----ASTLEGRRIIVADIGWP 406

Query: 308 EDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVG 367  
+ + G ++LG GE E ETE +L E+ V FS VL LP+ +PW+I ++  
Sbjct: 407 RNSRYPNGHFVRNLGDVGEKETETEVLLLEHDVPHQPFSQAVLSFLPK-MPWSITEKDMK 465

Query: 368 KRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAEE 427  
R DLR CI ++DP D+DDAL CR L +G EVGVHIADVS+F+ G++LD+ +A  
Sbjct: 466 NREDLRHLCSVDPPGCTDIDDALHCRELENGNLEVGVIADVSHFIRPGNALDQESAR 525

Query: 428 RATSIVLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRRTIIRSC 487  
R T+VYL +K + M+P LL LCSL D+L FS IW++ +IL+ F +++I S  
Sbjct: 526 RGTTVYLCEKRIDMVPELLSSNLCSLKCDVDRALAFSCIWEMNHNAEILKTKFTKSVINSK 585

Query: 488 TKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRRQRFVDGAL 547  
L+Y AQ I++ +++ ++ L+ +AK L+++R GAL  
Sbjct: 586 ASLTAEALRIDSANMN-----DDITSLRGLNKLAKILKKRIEKGAL 630

Query: 548 RLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRR 607  
L ++ F +D ET P E R++N +VEEFMLLAN++VA KI F E ALLR+  
Sbjct: 631 TLSSPEVRFHMDSETHDPIDLQTKELRETNMVEEFMLLANISVAKKIH EEFSEHALLRK 690

Query: 608 HPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLTNMYSRPM 667  
HP P LV+ L + +A +L +SL + L +L + +R M  
Sbjct: 691 HPAPPSNYEILVKAARSRL EIKTDTAKSLAESLDQAESPTFPYL--NTLLRILATRCM 748

Query: 668 QMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALG---YSEQP 723  
A+YFCSGM D F HY L P+YTHFTSPIRR+ADVIVHRLLA A+G Y E  
Sbjct: 749 MQAVYFCSGMDND---FHHYGLASPIYTHFTSPIRRYADVIVHRLLAIVAIGADCTYPELT 805

Query: 724 DVEPDTLQKQADHC---NDRRMASKRVQELSGLFFAVLVKESGPLESEAMVMGVNLQAF 780  
D K AD C N R ++ Q S+ + K G + EA ++ V A  
Sbjct: 806 DK-----HKLADICKNLNFRHKMAQYAQRASVAFHTQLFFKSKGIVSEEAYILFVRKNAI 860

Query: 781 DVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIFSLVDV 840  
VL+ ++G++ + F + KP L+++ + + V +F V V  
Sbjct: 861 VVLIPKYGLEGTV-----FFEEKDKPNPQLIYDDEIPSLKIEDTVFHVFDKVKV 909

Query: 841 VLQAEATA LKYS AI 854  
+ +++ L++ I  
Sbjct: 910 KIMLDSSNLQHOKI 923

Score = 50.1 bits (118), Expect = 2e-04  
Identities = 27/83 (32%), Positives = 48/83 (57%), Gaps = 5/83 (6%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFI---PSPDGDRDIFIDGVARNRA 105  
IF ++ + +G+K GT +QG R + + + EA + + +++I + G+ NRA  
Sbjct: 227 IFSEHLPLSKLQQGIKSGTYLQGTFRASRENYLEATVWIHGDSEENKEIILQGLKHLNRA 286

Query: 106 LNGDLVVVKLLPEDQWKAVKPES 128  
++ D+V V+LLP+ QW V P S  
Sbjct: 287 VHEDIVAVELLPKSQW--VAPSS 307

>gi|6324552|ref|NP\_014621.1| Possible component of RCC1-Ran pathway; Dis3p  
[Saccharomyces cerevisiae]  
gi|2500547|sp|Q08162|RR44\_YEAST Exosome complex exonuclease RRP44  
(Ribosomal RNA processing protein 44) (Protein DIS3)  
gi|2131990|pir|S66704 hypothetical protein YOL021c - yeast (Saccharomyces cerevisiae)  
gi|1419801|emb|CAA99021.1| ORF YOL021c [Saccharomyces cerevisiae]

gi|1754617|dbj|BAA11176.1| DIS3 protein [Saccharomyces cerevisiae]  
Length = 1001

Score = 321 bits (823), Expect = 3e-86  
Identities = 253/761 (33%), Positives = 364/761 (47%), Gaps = 99/761 (13%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGLRINPKKFHEAFIPSPDGDRIIDFIDGVVARNRALNGD 109  
F Y S V GLK G L QG ++I+ F E + P + + I G NRA NGD  
Sbjct: 255 FPEYYSTARVMGGLKNGVLYQGNIQISEYNFLEGSVSLPRFSKPVLIIVGQKNLNRANFNGD 314

Query: 110 LVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGSWSPDVIIIEAQF 169  
V+V+LLP+ +WKA D E H + + PD IEA  
Sbjct: 315 QVIVELLPQSEWKAPSSIVLDSE-----HFDVNDN-----PD--IEAG- 350

Query: 170 DDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQK 229  
DD D+ + NT+ + D ++L + KD I Q + K +Q  
Sbjct: 351 DDDNNNESSNTTIVISDKQRR-----LAKD--AMIAQRS-----KKIQP 388

Query: 230 SAKVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKD-CPQDFM 288  
+AKVVYI +++ R G LA + D P ++V L D C  
Sbjct: 389 TAKVVYI-QRRSWRQYVG---QLAPSSVD-----PQSSSTQNVFVILMDKCLPKVR 435

Query: 289 TRPKDFANTL---FICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDF 345  
R + A L + I W + LG + LG + ETE +L E+ V++ F  
Sbjct: 436 ITRRAAELLDKRIVISIDSWPTTHKYPLGHFVRDLGTIESAQAEATEALLLEHDEVEYRPF 495

Query: 346 SSEVLECLP-QSLPWTIP-----PDEVG-----KRRDLRKDCIFTIDPSTARDLDDALA 393  
S +VLECLP + W P P+ V KR+DLR I +IDP D+DDAL  
Sbjct: 496 SKKVLECLPAEGHDWKAPTCLDDPEAVSKDPLLTKRKDLRDKLICSIDPPGCVDIDDALH 555

Query: 394 CRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVPMPLPRLLCEELCSL 453  
++L +G +EVGVHIADV++FV G++LD A R TSVYLV K + MLP LL +LCSL  
Sbjct: 556 AKKLPGNWEVGVHIADVTHFVKPGTALDAEGAARGTSVYLVDKRIDMLPMLLGTDLCSL 615

Query: 454 NPMTDKLTFSVIWKLTPPEGKILEEWFGRITIRISCTKLSYDHAQSMIENXXXXXXXXXXXXX 513  
P D+ FSVIW+L I+ F +++IRS SY+ AQ I++  
Sbjct: 616 KPYVDRFAFSVIWELDDSANIVNVNFMKSIVIRSREAFSYEAQLRIDDKTQN----- 667

Query: 514 XXXXHSVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEY 573  
+E+ + L ++ +L+++R GAL L ++ +D ET P I +  
Sbjct: 668 -----DELTGMRRALLKLSVKLKQKRLEAGALNLASPEVKVHMDSETSDPNEVEIKKL 720

Query: 574 RDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPTKMLSDLVEFC-D-QMGLPMDV 632  
+N LVEEFMLLAN++VA KI+ FP+ A+LRRH P + L E + + + + +  
Sbjct: 721 LATNSLVEEFMLLANISVARKIYDAFPQTAMLRRAAPPSTNFEILNEMLNTRKNMSISL 780

Query: 633 SSAGALNKSLSLTKTFG-DDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNV 691  
S+ AL SL + +D Y ++ M +R M A YF SG FRHY L V  
Sbjct: 781 ESSKALADSLDRCDVPDPYF---NTLVRIMSTRCMAAQYFYSGAYS-YPDFRHYGLAV 836

Query: 692 PLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPD--TLQKQADHCNDRRMASKRVQE 749  
+YTHFTSPIRR+ DV+ HR LA A+GY D + + N + ++  
Sbjct: 837 DIYTHFTSPIRRYCDVVAHRQLAGAIGYEPLSLTHRDKNKMDMICRNINRKHNAQFAGR 896

Query: 750 LSIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQ 790  
SI + +++ + E+ V+ V N VLV +FGV+  
Sbjct: 897 ASIEYYVGQVMRNNESTET-GYVIKVFNNGIVVLVLPKFGVE 936

>gi|21297331|gb|EAA09476.1| ebiP3704 [Anopheles gambiae str. PEST]  
Length = 965

Score = 313 bits (803), Expect = 6e-84  
Identities = 228/691 (32%), Positives = 352/691 (50%), Gaps = 62/691 (8%)

Query: 180 NTSGLDVGKLSISTPDRGKEDSSTPVMKDENTPI-----PQDTRGLSEKSLQK-SAKV 233

N + VDG P+ + S V+ DE T P T + ++ ++ +AKV  
 Sbjct: 280 NLNRAVDGDTVAIEMLPESSEWKAPSDVVLVDEQTDPGDMVEPDPTFSVKPQAEREPTAKV 339  
 Query: 234 VYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKD 293  
 V I+++K R GIL + S +F P++ ++PRI + +  
 Sbjct: 340 VGIKRKW-RQYCGILLPSHIQGS----TRHIFVPAERKIPRIETRQ----- 383  
 Query: 294 FANTLFICRII----DWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEV 349  
 A TL RII W + G ++LG G E E E IL E+ V S FS +V  
 Sbjct: 384 -AATLLSQRIIIVADQWPRHSRYPOGHFVRALGPIGSKETENEVILLEDVPHSRFSEDV 442  
 Query: 350 LECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEYGVHIA 409  
 L CLP+ LPWTI ++ +R DLR + ++DP D+DDAL RRL +G EVGVHIA  
 Sbjct: 443 LACLPE-LPWTITAADLQRRVDLRDITVCSVDPPGCTDIDDALHARRLPNGNIEVGVHIA 501  
 Query: 410 DVSYFVPEGSSLDKVAERATSVYLQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLT 469  
 DV +F+ G++LD+ AA RAT+VYLV K + M+P LL LCSL ++ FS IW+L  
 Sbjct: 502 DVGHFIRPGTALDREAASRATTVYLVDKRIDMVPGLSSNLCSLRGGEERFAFSCIWELD 561  
 Query: 470 PEGKILEEWFGRTIIRCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLN 529  
 E I + +++I+S + L+Y+ AQ +I++ +V ++  
 Sbjct: 562 DEANIRNTRYHKSIVKSKSALTYEEAQIIDD-----AKQTNDVATSLRL 606  
 Query: 530 LHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANM 589  
 L+ +AK L+++R GAL L ++ F +D ET P + ++N +VEEFMLLAN+  
 Sbjct: 607 LNRLAKILKKRRTEKGALVLAPEIRFQVDSETHDPIDVKAQQLLETNSMVEEFMLLANV 666  
 Query: 590 AVAHKIFRTFPEQALLRRHPPQTKMLSDLVEFCQDQMLPMDVSSAGALNKSILTKTFGDD 649  
 +VA KI + FPE A+LRRHP P LV+ + G + +S L SL K D  
 Sbjct: 667 SVAEKIEQEFPECAMLRHPCPPQANYEPLVKA AEHQFEILTTSKELATSLDKAVKPD 726  
 Query: 650 KYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQRHYALNVPLYTHFTSPIRRFADVIV 709  
 +L + +R M A+YF SG +Q +++F HY L P+YTHFTSPIRR+AD+IV  
 Sbjct: 727 NPYF--NTMLRILATRCMMQAVYFISGTVQ-RDEFFHYGLAAPIYTHFTSPIRRYADIIV 783  
 Query: 710 HRLLAALGYSEQPDVEPDTLQKQADH--CND---RRMASKRVQELSIGLFFAVLVKESG 764  
 HRLLA +G P+ L K+ + CN+ R ++ S+ L + ++  
 Sbjct: 784 HRLLAACIGADS---TYPELLDKKVNSNLNLRNRMAQYAGRASVALHTHLFFRKRS 840  
 Query: 765 PLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWPEDDLE 824  
 + +A ++ + A +LV ++G + IY R+ K G + V++ +  
 Sbjct: 841 E-DEQAYILFIRKNALQILVPKYGFEGTIYVTG---RNNEEIKTGVR----FVYDEEQQT 892  
 Query: 825 EEPTQQVITIFSLVDVVLQAEATALKYSAIL 855  
 + Q V F V V L ++T +++ ++  
 Sbjct: 893 QRCGQVVFRAFDPVIVRLSLDSTNVQHEKLV 923

Score = 53.1 bits (126), Expect = 2e-05  
 Identities = 23/75 (30%), Positives = 46/75 (61%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNG 108  
 +F +++ + EG+K G L+QG + + + E ++ ++ + I G + NRA++G  
 Sbjct: 228 LFPShLTMLQIHGKIGGKLMQGGFLASRENYLEGYVRVEGIEKAVLIQGRMNLRNRAVDG 287  
 Query: 109 DLVVVKLLPEDQWKA 123  
 D.V +++LPE +WKA  
 Sbjct: 288 DTVAIEMLPESSEWKA 302

>gi|14250908|emb|CAC39259.1| Rrp44p homologue [Trypanosoma brucei]  
 Length = 972

Score = 313 bits (801), Expect = 1e-83  
 Identities = 187/536 (34%), Positives = 289/536 (53%), Gaps = 35/536 (6%)

Query: 265 LFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQA 324  
 LF P D+R+PRI + D + I DW E +F +G + LG  
 Sbjct: 396 LFQPKDNRIPIRIT-----TAHLGDLKDKRLSVIIDDWGEHSSFPVGHYVEVLGTI 447

Query: 325 GEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPST 384  
 G+ + E + IL E + DFS V +CLP+ W + +E+G R DLR C+ ++DP  
 Sbjct: 448 GDKDTEAKVILLENDIPHYDFSEAVYDCLPKG-EWNVTEEELGNRLDLRLDCVVSVDPLG 506

Query: 385 ARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPR 444  
 RD+DDAL CRR+ EVGVHIADV++F+ EG+++D+ AA+R+TSVYLV + + MLP+  
 Sbjct: 507 CRDIDDALHCRRVNGNHLEVGVIADVTHFLKEGTAMDEEAAKRSTSVYLVDRRINMLPQ 566

Query: 445 LLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWFGRTIIRSC TKLSYDHAQSMIENXXX 504  
 LL E LCS+ D+ FS++W+ ++ E+FG+T+IRS L Y AQ MI++  
 Sbjct: 567 LLTENLCSIVADEDRYAFSIMWEFDENYSVVRFFGKTVIRSRAALYYGDAQRMIDDPED 626

Query: 505 XXXXXXXXXXXXXHSVEEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGL 564  
 E ++ L +++ R++R DGAL L + F +D++  
 Sbjct: 627 E-----SEAAVSLRYLMQLSRHFRKRREKDGALFLCSQEFKFKVDNDHVN 671

Query: 565 PQGCHIEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPTKMLSDLVEFC- 623  
 P Y+ DSN ++EE+ML AN A A +++ +FP LLRRH P L E  
 Sbjct: 672 PTDMQAYQTFDSNSMIEEWMLFANAAAARRVYASFPRWTLRRHQAPAENAFDTLNEAIR 731

Query: 624 DQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQ 683  
 ++G+ +D +++ ALN+SL K R ++ + +R ++ A YF S + +++  
 Sbjct: 732 RKIGVKLDDTTSLALNESLEKCVDPSPDPYFNR--LIRTLVTRCLRQAQYFSSSEVS-KDE 788

Query: 684 FRHYALNVPLYTHFTSPIRRFADVIVHRLAALGYSEQPDVEPDTLQKQ--ADHCNDRR 741  
 F H+ L +P+YTHFTSPIRR+ADVIVHR LAAALG + + ++++ A + N R  
 Sbjct: 789 FHHFGLAMPIYTHFTSPIRRYADVIVHRQLAALGIMDVSEAHMVSVKMEALASNLNYRH 848

Query: 742 MASKRV---QELSIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRI 793  
 ++R Q L G + + P E +V F VLV ++G + +I  
 Sbjct: 849 EQAQAGRDSQNLFTGFYLRNFANQEIPSEDGYVVKLSETHVF-VLVPKYGQEGKI 903

Score = 40.0 bits (92), Expect = 0.17

Identities = 26/115 (22%), Positives = 52/115 (45%), Gaps = 9/115 (7%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGLRINPKKFHEAFIPSPDGD-----RDIFIDGVVAR 102  
 +F +++++ + G++ GT ++G LR++ F G + + G  
 Sbjct: 235 LFSPHLAESALDLGVQNGTYLRGKLRVSETN--CFFGEIRGQWKGNFERVLLPGRTNL 291

Query: 103 NRALNGDLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKG 157  
 NRA++GD+V V+LLP W+ ++ +E+ T E G + + +G  
 Sbjct: 292 NRAIHGDIVTVELLPVASWRPLRGAKPTEEMNDTGAGGDDHENSREGIGEESSEG 346

>gi|19113445|ref|NP\_596653.1| mitotic control protein dis3  
 [Schizosaccharomyces pombe]  
 gi|585053|sp|P37202|DIS3\_SCHPO Mitotic control protein dis3  
 gi|283075|pir||A41944 mitotic control protein dis3+ - fission yeast  
 (Schizosaccharomyces  
 pombe)  
 gi|173381|gb|AAA35302.1| mitotic control protein  
 gi|3650393|emb|CAA21102.1| mitotic control protein dis3  
 [Schizosaccharomyces pombe]  
 Length = 970

Score = 301 bits (770), Expect = 4e-80

Identities = 202/594 (34%), Positives = 301/594 (50%), Gaps = 43/594 (7%)

Query: 218 DTRGLSEKSLQKSAKVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIY 277  
 D +++++ +AKVV IL++ + ++ ++ L +P D RVP+I  
 Sbjct: 348 DLELITKRNAHPTAKVVGILKRNWRPYVGHVDNATIAQSKGGSQQTVLLTPMDRRVPKIR 407

Query: 278 VPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTE 337  
+ P+ R + I W + G + LG+ E ETE +L E  
Sbjct: 408 FRTRQAPRLVGRR-----IVVAIDLWDASSRYPEGHFVRDLGEMETKEAETEALLLE 459

Query: 338 YGVDFSDFSSEVLECLPQS-LPWTIPPDEV---GKRRDLRKDCIFTIDPSTARDLDDAL 392  
Y V F VL+CLP+ W +P D+ R+D R I +IDP +D+DDAL  
Sbjct: 460 YDVQHRPFPKAVLDCLPEEGHNWKPADKTHPLWKNRKDFRDKLICSIDPPGCQDIDDAL 519

Query: 393 ACRRLTDGTFEYGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEELCS 452  
L +G +EVGVHIADV++FV +S+D AA R T+VYLV K + MLP LL +LCS  
Sbjct: 520 HACVLPNGNYEYGVHIADVTHFVKPNTSMDSEASRGTTVYLVDKRIDMLPMLLGTDLCS 579

Query: 453 LNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRCTKLSYDHAQSMIENXXXXXXXXXXXX 512  
L P ++ FS IW++ I++ F +++I S SY AQ+ I++  
Sbjct: 580 LRPYVERFAFSCIWEMDENANIIKVHFTKSVIASKEAFSYADAQARIDDQKMQ----- 632

Query: 513 XXXXXHSVEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGGCHIYE 572  
+ + Q + L ++K L+++R +GAL L ++ D+ET P I +  
Sbjct: 633 -----DPLTQGMRVLLKLSKILKQKRMDEGALNLASPEVRIQTDNETSDPMDVEIKQ 684

Query: 573 YRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH-PPPQTKM--LSDLVEFCDQMGLP 629  
++N LVEEFMLLAN++VA KI+ FP+ A+LRRH PP T L D++ C M L  
Sbjct: 685 LLETNSLVEEFMLLANISVAQKIYDAFPQTAVLRRHAAPLTNFDLSQDILRVCKGMHLK 744

Query: 630 MDVSSAGALNKSLSLTKTFGD--DKYSLARKEVLTNMYSRPMQMALYFCSGMLQDQEQRHY 687  
D S KSL K+ + D +L + +R M A YFCSG + FRHY  
Sbjct: 745 CDT-----KSLAKSLDECVDPEPYFNTLLRILTTRCMLSAEYFCSGTFAPPD-FRHY 797

Query: 688 ALNVPLYTHFTSPIRRFADVIVHRLAAALGYSE-QPDV-EPDTLQKQADHCNDRRMASK 745  
L P+YTHFTSPIRR+ADV+ HR LAAA+ Y P + + L + + N R ++  
Sbjct: 798 GLASPIYTHFTSPIRRYADVLAHRQLAAAIYETINPSLSDKSRLIEICNGINYRHRMAQ 857

Query: 746 RVQELSIGLFFFAVLVKESGPLESEAMVMGVNLQAFDVLVLRFGVQKRIYCNALA 799  
SI + +K G E +A V+ V F V + RFG++ +Y +L+  
Sbjct: 858 MAGRASIEYYVGQALK-GGVAEEDAYVIKVFKNQGVVFIARFGLEGIVYTKSLS 910

Score = 49.7 bits (117), Expect = 2e-04  
Identities = 23/84 (27%), Positives = 46/84 (54%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRLNPKKFHEAFIPSPDGDGRDIFIDGVVARNRALNG 108  
++E + S + +K G + +G++ I+ + E + P ++ + + G NRA+ G  
Sbjct: 247 VYELHWSMSRLACIKNGEVHKGLINISTYNYLEGSVVVPGYNKPVLVSGRENLRNAVQG 306

Query: 109 DLVVVKLLPEDQWKAVKPESNDKE 132  
D+V +++LP+DQWK E D +  
Sbjct: 307 DIVCIQILPQDQWKTEAEEIADDD 330

>gi|15021874|dbj|BAB62212.1| hypothetical protein [Macaca fascicularis]  
Length = 249

Score = 291 bits (745), Expect = 3e-77  
Identities = 156/247 (63%), Positives = 171/247 (69%), Gaps = 2/247 (0%)

Query: 1 MNHPDYKLNLRXXIFETYMSKEDVS 60  
M+HPDY++NLR D IFETYM KEDVS  
Sbjct: 1 MSHPDYRMNLRPLGTGRGVSTVAGPHGIGASPGDKKSKNKSTRGKKKSIFETYMFKEDVS 60

Query: 61 EGLKRGTLIQGVLRLNPKKFHEAFIPSPDGDGRDIFIDGVVARNRALNGDLVVVKLLPEDQ 120  
EGLKRGTLIQGVLRLNPKKFHEAFIPSPDGDGRDIFIDGVVARNRALNGDLVVVKLLPE+Q  
Sbjct: 61 EGLKRGTLIQGVLRLNPKKFHEAFIPSPDGDGRDIFIDGVVARNRALNGDLVVVKLLPEEQ 120

Query: 121 WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQRKGWS-GPDVIEAQFDDSDSEDHRG 179  
WK VKPE+NDKE EA YE+DIPEE CG H QQS K ++ PDVIEAQFD SDSED HG

Sbjct: 121 WKVVKPENNDKETEAAYESDIPEELCGRHLPQQSLKSYNDSPDVIEAQFDGSDSEDGHG 180  
Query: 180 NTSG-LVDGVKKLSISTPDRGKEDSSTPVMKDENTPIQDTRGLSEKSLQSAKVVIILE 238  
T LVD VKKLS+ ++G+E PV KDE T I QDTR L EKSLQ+SAKV+  
Sbjct: 181 ITQNVLVDDVKKLSVCVSEKGREHGDAPVTKDETTTCISQDTRALPEKSLQRSACKVIAYRF 240

Query: 239 KKHSRAA 245  
H + A  
Sbjct: 241 SSHVQMA 247

>gi|19115966|ref|NP\_588616.1| hypothetical protein MGC4562 [Homo sapiens]  
gi|18314381|gb|AAH22089.1|AAH22089 Similar to mitotic control protein dis3  
homolog [Homo sapiens]  
Length = 971

Score = 284 bits (727), Expect = 4e-75  
Identities = 190/586 (32%), Positives = 297/586 (50%), Gaps = 50/586 (8%)

Query: 265 LFSPSDHRVPRIYVPLKDCP--QDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLG 322  
L +P D+R+P+I + + QDF + RI W+ + G + LG  
Sbjct: 283 LVTPWDYRIPKIRISTQQAETLQDFRV-----VVRIDSWESTSVYPNGHFVRVLG 332

Query: 323 QAGEIEPETEGILTEYGVDFSDFSSVELECLPQSL---PWTIPPDEVGKRRDLRKD-CIF 378  
+ G++E E IL E + FS + +P + PW + P+E KR+DLRK +F  
Sbjct: 333 RIGDLEGEIATILVENSISVIPFSEAQMCEMPVNTPESPWKVSPEEEQKRKDLRKSHLVF 392

Query: 379 TIDPSTARDLDDALACRRLTDGTFEVGVIADVSYFVPEGSSLDKVAERATSVYLVQKV 438  
+IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT+ YL +  
Sbjct: 393 SIDPKGCEDVDDTLSVRTLNNGNLELGVHIADVTHFVAPNSYIDIEARTRATYYLADRR 452

Query: 439 VPMLPRLLCHEELCSLNPMTDKLTFSVIWKLTPEG-KILEEWFGRTIIRSCTKLSYDHAQS 497  
MLP +L +LCSL D+ S++W+L +I + W+GRTIIRS KL Y+ AQ  
Sbjct: 453 YDMLPSVLSADLCSLLGGVDRYAVSIMWELDKASYEIKKVWYGRTIIRSAYKLFYEAQAE 512

Query: 498 MIENXXXXXXXXXXXXXXXXXHS----VEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQLK 553  
+++ S +EE+ A+ L IA+ +R +R GAL L+ ++  
Sbjct: 513 LLDGNLSVVDIDPEFKDLDEKSRQAKLEELVWAIGKLTDIARHVRAKRDGCGALELEGVE 572

Query: 554 LAFTLD-----HETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH 608  
+ LD H+ Q ++E V E M+LAN VA KI+ +FP QALLR+H  
Sbjct: 573 VCVQLDDKKNIHDLIPKQPLEVHE-----TVAECMILANHWVAKKIWESFPHQALLRQH 626

Query: 609 PPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLTNMYSRPMQ 668  
PPP + S+L E G +D S L SL +D + +L +M ++ M  
Sbjct: 627 PPPHQEFFSELRECAKAKGFFIDTRSNTKLADSLDN--ANDPHDPVNRLLRSMATQAMS 684

Query: 669 MALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPD 728  
ALYF +G +E+F HY L + YTHFTSPIRR++D++VHRLLAALGYSEQPDVEPD  
Sbjct: 685 NALYFSTGSCA-EEEFHHYGLALDKYTHFTSPIRRYSIDIVHRLLMAAISKDKKMEIKGN 743

Query: 729 -----TLQKQADHCNDRMASKRVQELSIGLFFAVLVKESGPLE-----SEAMVMGVNLQ 778  
L++ H N+R A++ Q+ S LF + K+ P S+ ++ +  
Sbjct: 744 LFSNKDLEELCRHINNRNQAQHSQKQSTELFQCMYFKDKDPATEERCISDGVIIYSIRTN 803

Query: 779 AFDVLVLRFVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLE 824  
+ + RFG++ Y L++ + P+ W+P L+  
Sbjct: 804 GVLLFIPRFGIKGAAY-----LKNKDGLVISCGPDCSEWKPGSLQ 844

Score = 59.3 bits (142), Expect = 3e-07  
Identities = 33/82 (40%), Positives = 51/82 (62%), Gaps = 8/82 (9%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFH-EAFI-----PSPDGD--RDIFIDGVVA 101  
+ ++ E + G+K G IQG+L +N + EAF+ S D D DI I G+ A  
Sbjct: 142 YPEHLPLEVLEAGIKSGRYIQGILNVNKHRAQIEAFVRLQGASSKSDSLVSDILIHGMKA 201



Query: 102 RNRALNGDLVVVKLLPEDQWKA 123  
RNR+++GD+VVV+LLP+++WK  
Sbjct: 202 RNRSIHGDVVVVVELLPKNEWKG 223

>gi|18916779|dbj|BAB85541.1| KIAA1955 protein [Homo sapiens]  
Length = 947

Score = 284 bits (726), Expect = 5e-75  
Identities = 190/586 (32%), Positives = 297/586 (50%), Gaps = 50/586 (8%)

Query: 265 LFSPSDHRVPRIYVPLKDCP--QDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLG 322  
L +P D+R+P+I + + QDF + RI W+ + G + LG  
Sbjct: 259 LVTPWDYRIPKIRISTQQAETLQDFRV-----VVRIDSWESTSVYPNGHFVRVLG 308

Query: 323 QAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSL---PWTIPPDEVGKRRDLRKD-CIF 378  
+ G++E E IL E + FS + +P + PW + P+E KR+DLRK +F  
Sbjct: 309 RIGDLEGEIATILVENSISVIPFSEAQMCEMPVNTPESPWKVSPREEQKRKDLRKSHLVF 368

Query: 379 TIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKV 438  
+IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT+ YL +  
Sbjct: 369 SIDPKGCEDVDDTLVSVRTLNNGNLELGVHIADVTHFVAPNSYIDIEARTRATTYYLADRR 428

Query: 439 VPMLPRLLCCELCSLNPMTDKLTFSVIWKLTPEG-KILEEWFGRTIIRSCTKLSYDHAQS 497  
MLP +L +LCSL D+ S++W+L +I + W+GRTIIRS KL Y+ AQ  
Sbjct: 429 YDMLPSVLSADLCSLLGGVDRYAVSIMWELDKASYEIKKVWYGRTIIRSAYKLFYEAQAE 488

Query: 498 MIENXXXXXXXXXXXXXXXXXHS----VEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQLK 553  
+++ S +EE+ A+ L IA+ +R +R GAL L+ ++  
Sbjct: 489 LLDGNLSVDDIPEFKDLDEKSRQAKLEELVWAIGKLTDIARHVRKRDGCGALELEGVE 548

Query: 554 LAFTLD-----HETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH 608  
+ LD H+ Q ++E V E M+LAN VA KI+ +FP QALLR+H  
Sbjct: 549 VCVQLDDKKNIHDLIPKQPLEVHE-----TVAECMILANHWVAKKIWESFPHQALLRQH 602

Query: 609 PPPQTKMLSDLVEFCQMGPLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLTNMYSRPMQ 668  
PPP + S+L E G +D S L SL +D + +L +M ++ M  
Sbjct: 603 PPPHQEFFSELRECAKAGFFIDTRSNTKTLADSLDN--ANDPHDPIVNRLLRSMATQAMS 660

Query: 669 MALYFCSGMLQDQEQRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPD 728  
ALYF +G +E+F HY L + YTHFTSPIRR++D++VHRLLA+ ++ +++ +  
Sbjct: 661 NALYFSTGSCA-EEEFHHYGLALDKYTHFTSPIRRYSDIVVHRLMAAISKDKKMEIKGN 719

Query: 729 -----TLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLE-----SEAMVMGVLNQ 778  
L++ H N+R A++ Q+ S LF + K+ P S+ ++ +  
Sbjct: 720 LFSNKDLEELCRHINNRRNQAAQHSQKQSTELFQCMYFKDKDPATEERCISDGVIIYSIRTN 779

Query: 779 AFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLE 824  
+ + RFG++ Y L++ + P+ W+P L+  
Sbjct: 780 GVLLFIPRFGIKGAAY-----LKNKDGLVISCSPDSCSEWKPGSLQ 820

Score = 59.3 bits (142), Expect = 3e-07  
Identities = 33/82 (40%), Positives = 51/82 (62%), Gaps = 8/82 (9%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFH-EAFI-----PSPDGD--RDIFIDGVVA 101  
+ ++ E + G+K G IQG+L +N + EAF+ S D D DI I G+ A  
Sbjct: 118 YPEHLPLEVLEAGIKSGRYIQGILNVNKHRAQIEAFVRLQGASSKSDLVSDILIHGMKA 177

Query: 102 RNRALNGDLVVVKLLPEDQWKA 123  
RNR+++GD+VVV+LLP+++WK  
Sbjct: 178 RNRSIHGDVVVVVELLPKNEWKG 199

>gi|27369724|ref|NP\_766107.1| hypothetical protein 4932411M14 [Mus musculus]

gi|26325912|dbj|BAC26710.1| unnamed protein product [Mus musculus]  
Length = 970

Score = 283 bits (724), Expect = 9e-75  
Identities = 194/595 (32%), Positives = 300/595 (50%), Gaps = 50/595 (8%)

Query: 265 LFSPSDHRVPRIYVPLK--DCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLG 322  
L + P D+R+P+I + + + QDF + RI W+ + G + LG  
Sbjct: 283 LVTPWDYRIPKIRISTQQAEALQDFRV-----VVRIDSWEATSVPNGHFVRVLG 332

Query: 323 QAGEIEPETEGILTEYGVDFSDFSSSEVLECLPQSL---PWTIPPDEVGKRRDLRKD-CIF 378  
+ G++E E IL E + FS + +P + PW + P E +R+DLR +F  
Sbjct: 333 RIGDLEGEIATILVENSISVVPFSEAQMCEMPVNTPENPWKVPKKEEQERKDLRTHLTF 392

Query: 379 TIDPSTARDLDDALACRRLTDGTFEVGVIADVSFVPEGSSLDKVAERATSVYLQKV 438  
+IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT+ YL +  
Sbjct: 393 SIDPKGEDVDDTLVRLNNGNLELGVHIADVTHFVAPNSYIDVEARTRATYYLADRR 452

Query: 439 VPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPPEG-KILEEWFGRTIIRSKLSYDHAQS 497  
MLP +L +LCSL D+ SV+W+L +I + W+GRTIIRS KL Y+ AQ  
Sbjct: 453 YDMLPSILSADLCSLLGGVDRYAVSVMWELDKTSYEIKKVWYGRTIIRSAYKLFYEAQE 512

Query: 498 MIENXXXXXXXXXXXXXXXXXHS---VEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQLK 553  
+++ S +EE+ A+ L IA+ +R +R GAL L+ ++  
Sbjct: 513 LLDGNFSIVDDIPELKALDKQSQAQKLEELVWAIGKLTDIARHIRAKRDRCGALELEGVE 572

Query: 554 LAFTLDHETGL-----PQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH 608  
+ LD + + Q ++E V E M+LAN VA KI+ +FP QALLR+H  
Sbjct: 573 VRVQLDDKKNIRDLPKQPLEVHE-----TVAECMILANHWVAKKIWESFPHQALLRQH 626

Query: 609 PPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVLTNMYSRPMQ 668  
PPP + S+L E G +D S L SL D K L K +L +M ++ M  
Sbjct: 627 PPPHQEFFSELRECAKAKGFFIDTRSNKTLADSLDSA-NDPKDPLVNK-LLRSMATQAMS 684

Query: 669 MALYFCSGMLQDQEQRHYALNVPLYTHFTSPIRRFADVIVHRLAAALGYSEQPDVEPD 728  
ALYF +G +E+F HY L + YTHFTSPIRR++D++VHRL AA+ ++ +++ +  
Sbjct: 685 NALYFSTGSCA-EEEFHHYGLALDKYTHFTSPIRRYSDIVHRLMAAISKDKMEIKEN 743

Query: 729 -----TLQKQADHCNDRMASKRVQELSIGLFFAVLVKESGPLESE-----AMVMGVLNQ 778  
L++ H N+R A++R Q+ S LF + K+ E ++ +  
Sbjct: 744 LFSNKNLEELCRHINNRRNRAAQRSQKQSTELFQCMYFKDRDAETEERCIADGVIYSIRTN 803

Query: 779 AFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVIT 833  
V + RFG++ Y L++ + PE + W+P L+ + + T  
Sbjct: 804 GVLVFIPRFGIKGAAY-----LKNKDSLVISCGPEGSSEWKPGSLQRSQNKIIST 853

Score = 54.7 bits (130), Expect = 7e-06  
Identities = 33/103 (32%), Positives = 54/103 (52%), Gaps = 8/103 (7%)

Query: 50 FETYMSKEDVSEGLKRGTLIQGVLRINPKKFH-EAFI-----PSPDGD--RDIFIDGVVA 101  
+ ++ E + G+K G IQG+L +N + EAF+ S D DI I G A  
Sbjct: 142 YPEHLPLEVLEAGIKSGRYIQGILNVNKHRAQIEAFVRLHGASSKDSGLVSDILIHGSKA 201

Query: 102 RNRALNGDLVVVKLLPEDQWKAVKPESNDKEIEATYEADIPEE 144  
RNR+++GD+VVV++LP+ +WK + + + + P E  
Sbjct: 202 RNRSIHGDIVVVEMLPKSEWKGRTAALGENDSDDKASGESPSSE 244

>gi|14250916|emb|CAC39263.1| putative ribonuclease II-like protein  
[Trypanosoma brucei]  
Length = 895

Score = 278 bits (710), Expect = 4e-73  
Identities = 236/763 (30%), Positives = 352/763 (46%), Gaps = 109/763 (14%)

Query: 52 TYMSKEDVSEGLKRGTLIQGLRI-NPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDL 110  
T S ++ + +K G ++ G LR+ + AF+ S D+ + G + NR. L+ D+  
Sbjct: 18 TIGSNPEMEKQVKHGCVVIGRLRVYSSYNSGLAFVRSGAFPADVVKGYGSINRFLHNDV 77

Query: 111 VVVKLLPEDQWKAV-----KPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVII 165  
V V+LLP +QW+ V +P+ +DK+ T D L R+ I  
Sbjct: 78 VAVQLLPMEQWEDVVSGELEPDGDDKDEFRTMRPD-----SERLPDGRR-----I 122

Query: 166 EAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEK 225  
D+ +R L + +S P P  
Sbjct: 123 TRWIRDTTMNNRKNREMWLAE-----MMSAPTEHNWHGKKP----- 158

Query: 226 SLQKSAKVYILEKKHSRAATGILKLLADKNSDLF--KKYALFSPSDHRVPRIYVPLKDC 283  
S V+ +LE+KH L A + ++ +++ F D +P I V +D  
Sbjct: 159 ----SGSVIAVLERKHPLLFVARLADDALSSQEVIQDRRFYRFKVFQDLLPHIAVFGDI 214

Query: 284 PQDFMTRPKDFANTLFICRI-----IDWKEDCNFALGQLAKSLGQAGEIEPETEGILT 336  
P F R + ++ R+ I W E F ++ + G + T I +  
Sbjct: 215 P--FSLR-ESIRERFYLLRLETTTGGDIVWAES-RFPTARIISTFGSVHSLRANTFAICS 270

Query: 337 EYGVDFSDFSSEVLECLPQSLPWTIPPDEVGK--RRDLRK-DCIFTIDPSTARDLDDAL 392  
+ + DFS E C+P L IP E K RDLR+ + + +IDP+TARDLDDAL  
Sbjct: 271 AHHIVTDDFSEEACNIPDRL--IIPNSEEMKRTGRDLRREEFVCSIDPATARDLDDAL 328

Query: 393 ACRRLTDGTFEYGVHIADVSFYFVEGSSSLDKVAAERATSVYLVQKVVPMLPRLLCEELCS 452  
+ L G + VGVHIADVS+FV GS+LD+ RATSIVLV +V MLPR L EE CS  
Sbjct: 329 SI-TLLPGGYRVGVHIADVSHFVSPGSALDEEGRARATSVYLVDRVYHMLPRKLSEYCS 387

Query: 453 LNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSC TKLSYDHAQSMIENXXXXXXXXXXXX 512  
L+P +DKL FS I++L GK+ EWFG+++IR+ +LSYD AQ +I+  
Sbjct: 388 LHPGSKLAFSAIFQLDLNGKLGGEWFGKSVIRNRCRLSYDDAQRIIDGNLTTLDALDYG 447

Query: 513 XXXXXHSVEE----VHQAVLNLHSIAKQLRRQRFVDGALRLDQLKLAFTLDHETG--LPQ 566  
+ + V +V +L +A +LR F G L ++ F + + P  
Sbjct: 448 GVTDRRELSQLKARVATSVKHLFDLASKLRAASFERGRALFSTPEIGFHFEDISNPTPI 507

Query: 567 GCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPPQTKMLSDLVEFCQDM 626  
G +++ ++N LVEEFMLLAN+ VA KI + P+QA+LR HPPP+ L ++  
Sbjct: 508 GFNVHRQIEANWLVEEFMLLANLRVAQKIVQYLPDQAILRVHPPPKRVPFEQL-----KV 562

Query: 627 GLP-MDVSSAGALNKS LTKTFGDDKYSLARKEVLTNMYSRPMQMALYFCSGM-LQDQE QF 684  
L +++ G NKSL + + R E+ + M + +A Y +G ++  
Sbjct: 563 SLARVNIELKGRSNKSLEQLLNSVRDHPLRDEI-SIMVKNLTLAKYCTNGENFTNKVPL 621

Query: 685 RHYALNPLYTHFTSPIRRFADVIHRLAAALGYSE-----QPDVEPDTL 730  
HYAL + YTHFTSPIRR+AD+IVHR L AL +E + L  
Sbjct: 622 GHYALGLEWYTHFTSPIRRYADIIVHRQLLCALEIESIVKGKHRTGKTCAGAVGMEVECL 681

Query: 731 QKQ-----ADHCNDRRMASKRVQELSIGLFFAVLVK 761  
AD CN+ + A+ V E S+ LFF +K  
Sbjct: 682 DSAEFFTSTYEVMMNIADECNENKRAADSVSEASLKLFFCHYLK 724

>gi|15559519|gb|AAH14124.1|AAH14124 Unknown (protein for IMAGE:4561365)  
[Homo sapiens]  
Length = 647

Score = 270 bits (689), Expect = 1e-70  
Identities = 178/534 (33%), Positives = 276/534 (51%), Gaps = 38/534 (7%)

Query: 315 GQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSL---PWTIPPDEVGKR RD 371  
G + LG+ G++E E IL E + FS + +P + PW + P+E KR+D  
Sbjct: 1 GTRVRVLGRIGDLEGEIATILVENSISVIPFSEAQMCEMPVNTPE SPWKVSPEEEQKRKD 60

Query: 372 LRKD-CIFTIDPSTARDLDDALACRRLTDGTFEYGVHIADVSFYFVEGSSSLDKVAAERAT 430  
LRK +F+IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT

Sbjct: 61 LRKSHLVFSIDPKGCEVDVDTLSVRTLNNGNLELGVHIADVTHFVAPNSYIDIEARTRAT 120

Query: 431 SVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPPEG-KILEEWFGRRTIIRSCTK 489  
 + YL + MLP +L +LCSL D+ S++W+L +I + W+GRRTIIRS K

Sbjct: 121 TYYLADRRYDMLPSVLSADLCSLLGGVDYAVSIMWELDKASYEIKKVWYGRRTIIRSAYK 180

Query: 490 LSYDHAQSMIENXXXXXXXXXXXXXXXXXHS----VEEVHQAVLNLHSLAKQLRRQRFVDG 545  
 L Y+ AQ +++ S +EE+ A+ L IA+ +R +R G

Sbjct: 181 LFYEAAQELLGDNLSVDDIPEFKDLGEKSRQAKLEELVWAIGKLTDIARHVRKRDGCG 240

Query: 546 ALRLDQLKLAFTLD-----HETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFP 600  
 AL L+ +++ LD H+ Q ++E V E M+LAN VA KI+ +FP

Sbjct: 241 ALELEGVEVCVQLDDKKNHDLIPKQPLEVHE-----TVAECMILANHWVAKKIWESFP 294

Query: 601 EQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLT 660  
 QALLR+HPPP + S+L E G +D S L SL +D + +L

Sbjct: 295 HQALLRQHPPPHQEFFSELRECAKAGFFIDTRS NKT LADSLD--ANDPHDP IVNRLLR 352

Query: 661 NMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYS 720  
 +M ++ M ALYF +G +E+F HY L + YTHFTSPIRR++D++VHRLL AA+

Sbjct: 353 SMATQAMS ANALYFSTGSCA-EEEFHHYGLALDKYTHFTSPIRRYS DIVVHRLLMMAISKD 411

Query: 721 EQPDVEPD-----TLQKQADHCNDRRMASKRVQELS IGLFFAVLVKESGPLE-----SEA 770  
 ++ +++ + L++ H N+R A++ Q+ S LF + K+ P S+

Sbjct: 412 KKMEIKGNLFSNKDLEELCRHINNRRNQAAQHSQKQSTELFQCMYFKDKDPATEERCISDG 471

Query: 771 MVMGVNLQAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEPDDLE 824  
 ++ + + + RFG++ Y L++ + P+ W+P L+

Sbjct: 472 VIYSIRTNGVLLFIPRFGIKGAAY-----LKNKDGLVISC GPDSCSEWKPGSLQ 520

>gi|23136616|gb|ZP\_00118334.1| hypothetical protein [Cytophaga  
 hutchinsonii]  
 Length = 750

Score = 265 bits (676), Expect = 3e-69  
 Identities = 168/466 (36%), Positives = 252/466 (54%), Gaps = 35/466 (7%)

Query: 315 GQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRK 374  
 G++ + LG AGE E E IL E+G+ + +F ++V++ Q + E+ KRRD+R

Sbjct: 219 GKVTEVLGMAGENETEMHAILAEFGLPY-EFPNQVIKA-AQDITAETSEAEIKKRRDMRG 276

Query: 375 DCIFTIDPSTARDLDDALACRRLTDGTFEYGVHIAVSYFVPEGSSLDKVAERATSVYL 434  
 FTIDP A+D DDA++ + L +G +E+GVHIAVSV++V G +LDK A RATSVYL

Sbjct: 277 TTTFTIDPEDAKDFDDAISFKYLDNGNWEIGVHIAVSHYVQPGDTLDKEAYRRATSVYL 336

Query: 435 VQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPPEGKILEEWFGRRTIIRSCTKLSYDH 494  
 V + VPMLP L ELCSL P DKLTFS I+++ + K+L+EWFGRTII S + SY+

Sbjct: 337 VDRCVPMLPERLSNELCSLRPNEDKLTFS AIFEIDADAKVLDEWFGRTIIHSTRRFSYEQ 396

Query: 495 AQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSLAKQLRRQRFVDGALRLDQLKL 554  
 AQ +IE ++ + + L+++AK++R QRF +GA+ + +++

Sbjct: 397 AQEVIETQQG-----DLVKELTILNTLAKKMRAQRFKEGAISFETVEV 439

Query: 555 AFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIF-----RTFPEQALLRRHP 609  
 F LD + G P +D++KL+EEFMLLAN VA +F + + R H

Sbjct: 440 KFQLDAK-GKPLAVVPKVRKDAHKLIEEFMLLANKRVAEFVFNLRKGKGTSTNTMVYRTHD 498

Query: 610 PPQTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLTNMYSRPMQM 669  
 P + L+ L F + G +++ A+ K+L K D+ + VL ++ R M

Sbjct: 499 APNPEKLASLATFAKRFQGHKVELDDENAIKLNK-LSDEVEGKPEQNVLSLAIRTMSK 557

Query: 670 ALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDT 729  
 A+Y E H+ L Y+HFTSPIRR+ DV+ HRL L + D E

Sbjct: 558 AIY-----SIEPDMHFGLAFFKHYSHTSPIRRYPDVMAHRLQLHYLDGGKSADKE--Y 608

Query: 730 LQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGV 775  
+ +H + + + + SI ++ S E E +V GV  
Sbjct: 609 YIEACEHSSAQEKLAEEAERSISKFKQVEFMQSSIGKEFEGIVSGV 654

>gi|19173030|ref|NP\_597581.1| similarity to DIS3 PROTEIN (RNASE II FAMILY)  
[Encephalitozoon  
cuniculi]  
gi|19168697|emb|CAD26216.1| similarity to DIS3 PROTEIN (RNASE II FAMILY)  
[Encephalitozoon  
cuniculi]  
Length = 835

Score = 260 bits (665), Expect = 6e-68  
Identities = 161/460 (35%), Positives = 240/460 (52%), Gaps = 64/460 (13%)

Query: 265 LFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQA 324  
L P D R+P I + ++ ++ N I W+ N+ G + LG  
Sbjct: 288 LVIPIDRRIPAIRIR-----TSQAEELMNKRLCVEIDGWERTSNYPGSHYYRLGTL 339

Query: 325 GEIEPETEGILTEYGVDFSDFS-SEVLECLPQSLPWTIPP-----DEV--GKRRDLR 373  
G+ E E +L G+ + + + +E+L +PW +EV G R D R  
Sbjct: 340 GDRNAEMEAVLVANGITYYNKNWAEILR-----VPWMNEDIFGMEKAYNEVREGTREDFR 394

Query: 374 KDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKVAERATSVY 433  
+ I +IDP D+DDAL CR L +G +EVGVHIADV+Y+V +GS +DK+AA+R T++Y  
Sbjct: 395 ELSIVSIDPPDCEDIDDALHCRLLPNGNWEVGVHIADVITYYVTGSEIDKIAADRGTITY 454

Query: 434 LVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEFGRITIRSC TKLSYD 493  
L + + MLP L +LCSL D+ FSV+W+++ + +++ F R++IRS SY+  
Sbjct: 455 LPEWRIDMLPPALSTDLC SLVAGKDRAAFSVVWEMSSDVRVVRTHFCRSLIRSKRSFSYN 514

Query: 494 HAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQLK 553  
A ++ +EV +++ L I++ LR +RF G+L L +  
Sbjct: 515 EAYDAVQGLVDAG-----DEVSRSLRMLLEISRVLRSRRFAKGSLLDSTRQ 560

Query: 554 LAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPT 613  
L F G + EY +N LVEEFM+LAN++VA I+ P+ +LLR+HPPP  
Sbjct: 561 LVFR-----EGGFEMKEYFPTNFLVEEFMVLANISVASFIYHHHPDSSLLRKHPPPSV 613

Query: 614 KMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLTNMYSRPMQMALYF 673  
+GL +D SS AL++SL K G RK++ M R M A+Y  
Sbjct: 614 L-----DIGLDIDTSSPRALSESLEKMEG-----VRKDLAKRMLIRSMNQAVYV 657

Query: 674 CSGMLQDQEQRHYALNVPLYTHFTSPIRRFADVIVHRL 713  
SG + HY L P+YTHFTSPIRR+AD+IVHR+L  
Sbjct: 658 VSG---ETPSLHHYGLATPIYTHFTSPIRRYADIIVHRIL 694

>gi|7493807|pir||T30524 protein phosphatase Ssd1 homolog - yeast (Candida albicans)  
gi|2459997|gb|AAC83386.1| protein phosphatase Ssd1 homolog [Candida albicans]  
Length = 1262

Score = 246 bits (628), Expect = 1e-63  
Identities = 230/859 (26%), Positives = 391/859 (45%), Gaps = 86/859 (10%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGVLRINPKKFHEAFIPSPDG--DRDIFIDGVVARNRAL 106  
+F Y+ + + E + G L+ G LR+N K +A++ S DG D DIFI G RNRAL  
Sbjct: 336 LFAPYLPQSSLPELINEGRVLTGTLRVNKKNRSDAYV-STDGLLDADIFICGSKDRNRAL 394

Query: 107 NGDLVVVKLLPEDQ-WKAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSPDVII 165  
GDLV V+LL D+ W++ K + K + P H+ S P+  
Sbjct: 395 EGD LVAVELLIVDEVWESKKEKEKKRRKDNTLHSRPLTDDIHN-----DATSAPNT-A 447

Query: 166 EAQFDDSDSEDRHGNTSGLVDGVKKLSISTPDRGKEDSSTPVMKDENTPIP-QDTRGLSE 224

E + ED G+ G+ + RG + K+++ + Q + E  
 Sbjct: 448 EGSVTGTSTKEDGAGSNEEETGGLAR-----RGS LKQRPTMKKNDDVEVEGQSLLLLVEE 500  
 Query: 225 KSLQKSAK-----VVYILEKKHSAATGILKLL-----ADK-----NSDLFK 261  
 + + K VV +++ + G L LL DK +  
 Sbjct: 501 EEINDEIKPLYAGHVAVVDRI PGQLFAGTLGLLRPAQAAQAARDKNGKESTVQNPKAP 560  
 Query: 262 KYALFSPSDHRVPRIYVPLKDCPDQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSL 321  
 K F P+D +VP I +P + P+DF+ + +A+ LF+ I W G L +L  
 Sbjct: 561 KIVWFKPTDKKVPLIAIPTEQAPKDFVENHEKYADRLFVASIKRWPITS LHPFGTLVSNL 620  
 Query: 322 GOAGEIEPETEGILTEYGVDFSDFS----SEVLECLPQSLPWTIPPDEVGKRRDLRKDCI 377  
 G E E + IL + ++ +++ LP P E +R + D I  
 Sbjct: 621 GPIDSPETEIDSILRDNNFLCDEYPDDDNDDIVSVNAYDLPSIEPEFENTQREEYLNDYI 680  
 Query: 378 FTIDPSTARDLDDALACRRLTDGTFEYGVHIADVSYFVPEGSSLDKVAERATSVYLQK 437  
 +D AL +R+++ E+G H+AD++YF+ GSSLD+ + +R++SV+L QK  
 Sbjct: 681 IAFT-QNGEFDHALHVKRISNTKIELGFHVADIAYFIKPGSSLDKRSKRSVFLPQK 739  
 Query: 438 VVPMLPRLLCEELCSLNPMTDKLTFSVIWKL-TPEGKILEEWFGRTIIRSCTKLSYDHAQ 496  
 V + P+ + ++ S L SV++++ T ++ + + ++I ++YD  
 Sbjct: 740 TVNLFQKQV-NKIVSFKENEKNLAVSVVFEIDTSNFEVEDLYIHESVIIPKQLVTYDAFD 798  
 Query: 497 SMIENTXXXXXXXXXXXXXXXXXHSVEEVHQA----VLNLHSIAKQLRRQRFVDGALRLD-Q 551  
 +++ SV+ + A V IAK+ RR R + +L +  
 Sbjct: 799 TILSG-----QSVDSISSATSDYVKTFSLIAKEFRRHRLSNRSLGITPN 842  
 Query: 552 LKLAFTLDHETGLPQGCHIYERDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPP 611  
 L L LD E + +I++ + ++ E N A+A K+ +QA+LRRHP P  
 Sbjct: 843 LTLLDQLDDEK-VRLDLNIFKDSLAFDVI SEISHKVNSAIAAKVHAGLDQAILRRHPLP 901  
 Query: 612 QTKMLSDLVEFCQMG LPM DVSSAGALNKS LTKTFGDDKYSLARKEVL TNMYSRPMQMAL 671  
 + + V +G +D +++ L S+ K DD + RK V T +Y + M  
 Sbjct: 902 TLQKMETFVRKATSLGFKIDTTTSTLQNSILKI--DD--PVKRKCVETLLY-KCMSRGR 956  
 Query: 672 YFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLAAALGYSEQPDVEPDTLQ 731  
 Y+ +G QD + + HY N+PLYTHFT+P+RR+AD+IVHR L A L + D + D+L+  
 Sbjct: 957 YYVAGK-QDTSYAHYYFNLPLYTHFTAPLRRYADLIVHRQLKAVLN-KQVEDKDLDLSLK 1014  
 Query: 732 KQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVNLQ----AFDVLVLR 787  
 D+CN ++ + QE +I L + + E + + MG + Q +FDV + F  
 Sbjct: 1015 AITDYCNFKKDCANAQEQAIHLLLSQTINEMSETAGQLLCMGTVVQVYESSFDVFIPEF 1074  
 Query: 788 GVQKRIYCINALALRSYSFQKVGKKPELTLVWEP--DDLEEEPTQQVITIFSLVDVVLQAE 845  
 GV+KR++ + L L F K + L L WE D P + ++ + +  
 Sbjct: 1075 GVEKRVHGDQLPLVKAEDFK--NERILELWWEKGVDSATYIPPDEKSSLSYRNSIKNKYR 1132  
 Query: 846 ATALKYSAILKRPGLKAS 864  
 +AL+ + I + LEK++  
 Sbjct: 1133 TSALQAQAIQSKTALEKST 1151

>gi|22748821|ref|NP\_689596.1| hypothetical protein MGC42174 [Homo sapiens]  
 gi|20988352|gb|AAH30113.1| similar to Hypothetical 93.7 kDa protein  
 F48E8.6 in chromosome III  
 [Homo sapiens]  
 Length = 159

Score = 242 bits (617), Expect = 2e-62  
 Identities = 119/135 (88%), Positives = 127/135 (94%)

Query: 727 PDTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKESGPLESEAMVMGVNLQAFDVLVLR 786  
 PDTLQKQADHCND RMASKRVQELS LFFAVLVKESGPLESEAMVMG+L QAFDVLVLR  
 Sbjct: 3 PDTLQKQADHCNDSRMASKRVQELSTSLFFAVLVKESGPLESEAMVMGILKQAFDVLVLR 62  
 Query: 787 FGVQKRIYCINALALRSYSFQKVGKKPELTLVWEPDDLEEEPTQQVITIFSLVDVVLQAEA 846

+GVQKRIYCNALALRS+ FQKVGKKPELTLVWEP+D+E+EP QQVITIFSLV+VVLQAE  
Sbjct: 63 YGVQKRIYCNALALRSHHFQKVGKKPELTLVWEPEDMEQEPAQQVITIFSLVEVVLQAEY 122

Query: 847 TALKYSAILKRPGLE 861

TALKYSAILKRPG +

Sbjct: 123 TALKYSAILKRPGTQ 137

>gi|27685983|ref|XP\_237349.1| similar to hypothetical protein MGC37640 [Mus  
musculus] [Rattus  
norvegicus]  
Length = 1034

Score = 241 bits (614), Expect = 5e-62

Identities = 117/128 (91%), Positives = 121/128 (94%), Gaps = 2/128 (1%)

Query: 188 VKKLSISTPDRGKEDSSTPVMKDENTPIPDTRGLSEKSLQSAKVYVILEKKHSRAATG 247

+KK+S S+ DR KEDSS PVMKDENTP QDTR LSEKSLQSAKVYVILEKKHSRAATG

Sbjct: 509 LKKIS-SSNDR-KEDSSAPVMKDENTPKSQDTRALSEKSLQSAKVYVILEKKHSRAATG 566

Query: 248 ILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDFANTLFICRIIDWK 307

ILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKD+ANTLFICRIIDWK

Sbjct: 567 ILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRPKDYANTLFICRIIDWK 626

Query: 308 EDCNFALG 315

EDCNFALG

Sbjct: 627 EDCNFALG 634

Score = 142 bits (357), Expect = 3e-32

Identities = 64/80 (80%), Positives = 70/80 (87%)

Query: 122 KAVKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSPDVIIIEAQFDDSDSEDRHGNT 181

+ VKPESNDKE EAT E DI EE CGHH LQ+S KGW+GPDVIIIEAQFDDSDSEDRHGNT

Sbjct: 328 RGVKPESNDKETEATNETDISEESCGHHLLQKSPKGNWGPDVIIIEAQFDDSDSEDRHGNT 387

Query: 182 SGLVDGVKKLSISTPDRGKE 201

SGLVDG+KKLS+ TPD+G E

Sbjct: 388 SGLVDGMKKLSVCTPDKGSE 407

Score = 127 bits (320), Expect = 6e-28

Identities = 58/62 (93%), Positives = 60/62 (96%)

Query: 316 QLAKSLGQAGEIEPETEGILTEYGVDIFSDFSSSEVLECLPQSLPWTIPPDEVGKRRDLRKD 375

QLAKSLGQAGEIEPETEGILTEYGVDIFSDFSSSEVLECLPQSLPWTIPP+EVGKRRDLR

Sbjct: 724 QLAKSLGQAGEIEPETEGILTEYGVDIFSDFSSSEVLECLPQSLPWTIPPDEVGKRRDLRSL 783

Query: 376 CI 377

C+

Sbjct: 784 CL 785

Score = 117 bits (292), Expect = 9e-25

Identities = 52/57 (91%), Positives = 57/57 (100%)

Query: 68 LIQGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDLVVVKLLPEDQWKAV 124

+++GVLRLINPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDLVVVKLLPEDQWK++

Sbjct: 205 VLKGVLRINPKKFHEAFIPSPDGRDIFIDGVVARNRALNGDLVVVKLLPEDQWKSL 261

Score = 60.1 bits (144), Expect = 2e-07

Identities = 25/28 (89%), Positives = 28/28 (100%)

Query: 373 RKDCIFTIDPSTARDLDDALACRRLTDG 400

+KDCIFTIDPSTARDLDDAL+CR+LTDG

Sbjct: 867 QKDCIFTIDPSTARDLDDALSCRQLTDG 894

>gi|6320499|ref|NP\_010579.1| Product of gene unknown; Ssd1p [Saccharomyces cerevisiae]  
gi|134917|sp|P24276|SSD1\_YEAST SSD1 PROTEIN (SRK1 PROTEIN)  
gi|101639|pir|A39578 SSD1 protein - yeast (Saccharomyces cerevisiae)  
gi|172612|gb|AAA35047.1| SSD1 protein  
gi|172697|gb|AAA35089.1| SRK1  
gi|1230657|gb|AAB64469.1| Ssd1p [Saccharomyces cerevisiae]  
Length = 1250

Score = 221 bits (564), Expect = 3e-56

Identities = 227/823 (27%), Positives = 369/823 (44%), Gaps = 95/823 (11%)

Query: 49 IFETYMSKEDVSEGLKRGTLIQGLRINPKKFHEAFIPSPDG--DRDIFIDGVVARNRAL 106  
+F Y+ + ++ E ++ G L+ G+LR+N K +A++ S DG D DI+I G RNRAL  
Sbjct: 340 LFAPYLPQANIPELIQEGRLVAGILRVNKKNRSDAWV-STDGALDADIYICGSKDRNRAL 398

Query: 107 NGDLVVVKLL-PEDQWKA-VKPESNDKEIEATYEADIPEEGCGHHPLQQSRKGWSGPDVI 164  
GDLV V+LL +D W++ + E + +A+ + D+ PL S + V  
Sbjct: 399 EGDLVAVELLVDDVWESKKEKEKKRRKDASMQHDLI-----PLNSSDDYHNDASVT 451

Query: 165 IEAQFDDSDSEDHRGNTSGLVDGVKKLSISTPDRGKEDSSTPV-----MKDENTPI 215  
+ S + S V++ ST + + S+P +K T  
Sbjct: 452 AATSNNFLSSPSSSDSLSKDDL SVRRKRSTINNDSDSLSSPTKSGVRRRSSLKQRPTQK 511

Query: 216 PQDTRGLSEKSL-----QKSAKVYILEKKHSRAATGILKLL---ADKNSD 258  
D + +SL + VV +L++ + +G L LL NSD  
Sbjct: 512 KNDDVEVEGQSLLLVEEEEINDKYKPLYAGHVAVLDRI PGQLFSGTLGLLRPSQQANS 571

Query: 259 LFK----KYALFSPSDHRVPRIYVPLKDCPDQDFMTRPKDFANTLFICRIIDWKEDCNFA 313  
K K A F P+D +VP I +P + P+DF+ ++ LF+ I W  
Sbjct: 572 NNKPPQSPKIAWFKPTDKKVLIAIPTELAPKDFVENADKYSEKLFVASIKRWPITSLHP 631

Query: 314 LGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLEC-----LPQSLPWTIPPDEVG 367  
G L LG + + E + IL D + S+E L+ P P + ++  
Sbjct: 632 FGILVSELGDIHDPDTEIDSILR----DNNFLSNEYLDQKNPQKEKPSFQPLPLTAESLE 687

Query: 368 KRR---DLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGSSLDKV 424  
RR D + IF I + AL R +GT E+G H+ DV+ + EGSS+D+  
Sbjct: 688 YRRNFTDTNEYNIFAIS-ELGWVSEFALHVRNNGNGTLELGCHVVDVTSHIEEGSSVDRR 746

Query: 425 AAERATSVYLQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPPEG-KILEEWFGRTI 483  
A +R+++V++ QK+V +LP+ +EL SL P + T SV++ L +I W G +  
Sbjct: 747 ARKRSSAVFMPQKLVNLLPQSFNDEL-SLAPGKESATLSVVYTLDSSTLRIKSTWVGEST 805

Query: 484 IRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRRQRFV 543  
I LS + + S + + IA+ +R  
Sbjct: 806 ISPSNILSLEQLDEKL-----STGSPTSYLSTVQEIARSFYARRIN 846

Query: 544 D-GALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQ 602  
D A L L'L +LD E + +I + ++ E N VA KI+ +  
Sbjct: 847 DPEATLLPTLSLLES LDDEK-VKVDLNLDRTLGFVVINEIKRVNSTVAEKIYTKLGDL 905

Query: 603 ALLRRHPPPTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVLTNM 662  
ALLRR P ++ + G D ++A L K + K DD R + +  
Sbjct: 906 ALLRRQMPIATKMASFRKKIQNFYNFDTNTADELIKGV LKIKDDD---VRVGIEILL 961

Query: 663 YSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQ 722  
+ + M A YF +G + D +Q+ HYALN+P+YTHFT+P+RR+AD +VHR L A + +  
Sbjct: 962 F-KTMPRARYFIAGKV-DPDQYGHYALNLPYTHFTAPMRRYADHVVRHQLKAVI--HDT 1017

Query: 723 PDVEP-DTLQKQADHCNDRRMASKRVQELSIGLFFAVLVKE----SGPSEAMVMGVLN 777  
P E + L+ +++CN ++ + + QE +I L + + +G L + A V+ V  
Sbjct: 1018 PYTEDMEALKITSEYCNFKKDCAYQAQEQAIHLL LCKTINDMGNTTGQLLTMATVLQVYE 1077



Query: 778 QAFDVLVLRFGVQKRIYCNALALRSYSFQKVGKKPELTLVWEP 820  
+FDV + FG++KR++ + L L F G L L W+P  
Sbjct: 1078 SSFDVFIPEFGIEKRVHGDQLPLIKAefd--GTNRVLELHWQP 1118

>gi|15616115|ref|NP\_244420.1| ribonuclease R; virulence-associated protein  
[Bacillus halodurans]  
gi|25298858|pir||A84094 virulence-associated protein BH3553 [imported] -  
Bacillus  
halodurans (strain C-125)  
gi|10176177|dbj|BAB07272.1| ribonuclease R [Bacillus halodurans]  
Length = 771

Score = 214 bits (545), Expect = 5e-54  
Identities = 163/515 (31%), Positives = 250/515 (48%), Gaps = 47/515 (9%)

Query: 232 KVVYILEKKHSRAATGILKLLADKNSDLFKKYALFSPSDHRVPRIYVPLKDCPQDFMTRP 291  
KV+ ILE R + ++ D + Y L D R+P + + Q +  
Sbjct: 127 KVIRILE---RGVSEVIGTYVDHQT-----YGLVVADDKRIPNDILIVNPEAQGLVDGH 177

Query: 292 KDFANTLFIICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLE 351  
K I + I + E A G++ LG + + I+ +YG+ F EVL+  
Sbjct: 178 K-----VIVKITYPEGRMSAEGEVISILGHKNDPGMDILSIYKYGIP-QAFPEEVLQ 230

Query: 352 CLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADV 411  
Q++P I E+ RRDLR + + TID + A+DLDDA+ RL +G F++GVHIADV  
Sbjct: 231 -QAQNIPDEIDAGEIKNRRDLRDEPLVTIDGADAKDLDDAVHSRLPNGNFKLGVHIADV 289

Query: 412 SYFVPEGSSLDKVAERATSYYLVQKVPMPLRLLCEELCSLNPMTDKLTFSVIWKLTP 471  
SY+V E S +D AAER TSVYLV +V+PM+P L +CSLNP D+LT S ++T +  
Sbjct: 290 SYYVKEKSPIDLEAAERGTSYYLVDRVIPMIPHRLSNGICSLNPQVDRLTLSCEMEITRD 349

Query: 472 GKILEEWFGRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXXXXHSEVEVHQAVLNH 531  
G+++ ++IR+ ++Y ++ +EE  
Sbjct: 350 GQVVNHEIFQSVIRTNERMTYHDVNKILVEKEEELRNRYELLVPMFEDMEE----- 400

Query: 532 SIAQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAV 591  
+A LR++RF GA+ D K A L E G P I E + KL+EEFML AN V  
Sbjct: 401 -LAAILRKKRFRGAIDFD-FKEAKVLVDEEGKPSDVIRERGVAEKLIIEFMLAANETV 458

Query: 592 AHKIFRTFPEQALLRRHPPPQTKMLSDLVEFCQMGPMQDVSSAGALNKS�TKTFGDDKY 651  
A F + R H P ++ L +EF G + ++ ++L K ++  
Sbjct: 459 AEH-FHWLKLPPMYRIHEDPDSEKLGRFLEFITNFGYVVRGTANTVHPRALQKLL-BEVR 516

Query: 652 SLARKEVLTNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHR 711  
++V++ + R MQ A Y D H+ L+ YTHFTSPIRR+ D+IVHR  
Sbjct: 517 GEPEEQVISTVMLRSMQQAQY-----DPTSLGHFGLSTEFYTHFTSPIRRYPDLIVHR 569

Query: 712 LLAAALGYSEQPDVEPDTLQKQ-----ADHCND 739  
L+ Y + +V+ +T +K A HC++  
Sbjct: 570 LIRE---YLIKGNVDEETQEKWRERLPEIARHCSE 601

>gi|23099883|ref|NP\_693349.1| ribonuclease R [Oceanobacillus iheyensis]  
gi|22778114|dbj|BAC14384.1| ribonuclease R [Oceanobacillus iheyensis]  
Length = 744

Score = 209 bits (533), Expect = 1e-52  
Identities = 140/418 (33%), Positives = 214/418 (51%), Gaps = 22/418 (5%)

Query: 300 ICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPW 359  
I RI + E N A G++ LG + + I+ ++G+ DF +VLE Q P  
Sbjct: 183 IARISKYPEGRNSAEGEIHHILGHKNDPGIDILSIHKKHGIQV-DPFDVLE-QAQQTPE 240

Query: 360 TIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGS 419  
I PDE+ RRDLR + I TID + A+DLDDA+ ++L++G +++GV+IADVS++V E S

Sbjct: 241 EIHPDEINGRRDLRNETIVTIDGADAKDLDDAVTVKKLSNGNYKLGVIADVSHYVKEES 300

Query: 420 SLDKVAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWF 479  
+D+ A ER TSVYLV +V+PM+P L +CSLNP D+LT ++ +G+++E

Sbjct: 301 PIDREALERGTSVYLVDRVIPMIPHRLSNGICSLNPKVDRRLTLCCEMEINHQQGVVEHEI 360

Query: 480 GRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHLSIAKQLRR 539  
+++I S +++Y ++ + +E NL SI LR

Sbjct: 361 FQSVIHSTERMTYSDVNKILVDQDEELRDKYEPLVPMFEEME-----NLASI---LRE 410

Query: 540 QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTF 599  
+RF GA+ D K A L + G P I E + +L+EEFML AN +A F

Sbjct: 411 KRFGRGAIQDFD-FKEAQLVDDMGRPTDVAIRERSVAERLIEEFMLAANETIAEH-FHWM 468

Query: 600 PEQALLRRHPPPTKMLSDLVEFCDQMGLPMDVSSAGALNKSLSLTKTFGDDKYSLARKEVL 659  
+ R H P L +F +G+ + +AG ++ + D + ++

Sbjct: 469 DVPFIHRIHEEPDEGKLEKFFDFLAGLGISVK-GTAGDIHPQELQKVIDSIRGEPEEMIV 527

Query: 660 TNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLAAAL 717  
+ + R MQ A Y D + H+ L YTHFTSPIRR+ D+IVHRL+ L

Sbjct: 528 SKMLLRSMQQAQY-----DPQSIGHFGLATDFYTHFTSPIRRYPDLIVHRLIRTYL 578

>gi|21673344|ref|NP\_661409.1| ribonuclease II family protein [Chlorobium  
tepidum TLS]  
gi|21646438|gb|AAM71751.1| ribonuclease II family protein [Chlorobium  
tepidum TLS]  
Length = 720

Score = 208 bits (529), Expect = 4e-52  
Identities = 155/466 (33%), Positives = 233/466 (50%), Gaps = 57/466 (12%)

Query: 265 LFSPSDHRV-PRIVPLKDCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQ 323  
L P ++ P I++PLK + K A L + ++ + LG

Sbjct: 154 LLKPDQRKILPEIHIPLKAAKKAKAG-DKVLAGELEFLK-----SGTIQARVIEILGT 205

Query: 324 AGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPS 383  
AGE + E I G+D F E+L + + I +++ +R D+R +FTIDP

Sbjct: 206 AGESQVEVSAIARGLGID-ETFEPELL-TFAEKVREAITDEDLKERLDIRDKDVFIDPV 263

Query: 384 TARDLDDALACRLTD-GTFEVGVIADVSYFVPEGSSLDKVAERATSVYLVQKVVPML 442  
A+D DDAL+ L + G ++VGVIADV++VPE S+LDK A +RATSVYLV +V+PML

Sbjct: 264 DAKDFDDALSIEITLGNNGGYKGVGVIADVSHYVPENSALDKEARKRATSVYLVDRVIPML 323

Query: 443 PRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRRTIIRSCTKLSYDHAQSMIENX 502  
P L E++CSLNP D+L FSV + +T +G++ + F +T+I S + +Y+ Q +++

Sbjct: 324 PSRLSEKVCSLNPGVDRDLAFSVFFNITKKGEVTKFEFHKTVIHSKRRFTYEDVQQILDAG 383

Query: 503 XXXXXXXXXXXXXXXXHSVEEVHQAVLNLHLSIAKQLRRQRFVDGALRLDQLKLAFTLDHET 562  
+ + + L ++K++R QR G L + ++ F L

Sbjct: 384 KG-----DYFRELQALDQLSKKIRAQRMESGGLEFETEEVRFKLG-SN 425

Query: 563 GLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTF-----PEQALLRRHPPPTKML 616  
G P E DS++L+EEFMLLAN VA + + P + R H PQ + +

Sbjct: 426 GEPVEVIKKERLDLHRLIEEFMLLANRTVAAYLTARYAENEKNPHPIYRVHGAPQMEKV 485

Query: 617 SDLVEFCDQMGLPMDVSSAG-----ALNKSLSLTKTFGDDKYSLARKEVLTNMYSRPM 667  
L F ++G + + G AL + L K G + L + VL R M

Sbjct: 486 QVLASFVRKIGFDLKLDRKGKDSATVSSKALRELLQKVRGTNVEFLVNLVL-----RSM 540

Query: 668 QMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRL 713  
A+Y L D H+ L YTHFTSPIRR+ D+IVHR+L

Sbjct: 541 SKAVY---SPLNDG---HFGLGFEHYTHFTSPIRRYPDLIVHRL 579

>gi|15672924|ref|NP\_267098.1| ribonuclease [Lactococcus lactis subsp.  
lactis]

gi|18202798|sp|Q9CH00|RNR1\_LACLA Ribonuclease R 1 (RNase R 1) (VacB protein homolog 1)  
 gi|25298855|pir||F86742 ribonuclease [imported] - Lactococcus lactis subsp. lactis (strain IL1403)  
 gi|12723878|gb|AAK05040.1|AE006328\_8 ribonuclease [Lactococcus lactis subsp. lactis]  
 Length = 817

Score = 206 bits (525), Expect = 9e-52  
 Identities = 137/421 (32%), Positives = 223/421 (52%), Gaps = 27/421 (6%)

Query: 315 GQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRK 374  
 G + + +GQA + + +L + S+F EVL+ +++P +P +E+ R D R  
 Sbjct: 207 GLVTEIIGQADDQGIDVLEVLASMDI-VSEFPKEVLD-QAEAVPEEVPENEIVGRVDYRN 264

Query: 375 DCIFTIDPSTARDLDDALACRRLTDGTFEVGVIADVSFYFVPEGSSLDKVAAERATSVYL 434  
 + FTID + A+DLDDA+ +RL +G +E+GVHIADVS++V E S LDK A ER TSVY+  
 Sbjct: 265 EITFTIDGADAKDLDDAVHAKRLENGNYELGVHIADVSHYVTENSPLDKEAYERGTSVYV 324

Query: 435 VQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRTIIRSCTKLSYDH 494  
 +VVPMLP L +CSLNP ++LT S + +++PEG+++ ++II++ +++YD  
 Sbjct: 325 TDRVVPMLPERLSNGICSLNPRINRLTQSCVMEISPEGRVINYQISQSIKTTTERTYDA 384

Query: 495 AQSMIENXXXXXXXXXXXXXXXXXSVVEVHQAVLNLSIAKQLRRQRFVDGALRLDQLKL 554  
 MI + + + ++ LH I + +R++R GA+ D ++  
 Sbjct: 385 VNQMIAGDEAALENYA-----KIADSVKIMVELHHILEAMRKRR---GAIDFDTVE- 432

Query: 555 AFTLDHETGLPQGCHIEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPQTK 614  
 A + +E GLP + +++E FML AN VA F + R H P+  
 Sbjct: 433 AKIIVNEKGLPIEIRKTRGIAERMIESFMLEANETVATH-FEAHGLPFIYRIHEQPKAD 491

Query: 615 MLSDLVEFCDQMGLPMDVSSAGALNKSLTKTFGDDKYSLARKEVLTNMYSRPMQMALYFC 674  
 L ++F G+ ++ +S G +++ + + F + VL+ M R MQ A Y  
 Sbjct: 492 RLQRFIDFAATFGMQIEGTSNG-IDQKVLQAFMKKIKGQPGEMVLSTMLLRSMQQARY-- 548

Query: 675 SGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDVEPDTLQKQA 734  
 + H+ L YTHFTSPIRR+ D++VHRL+ +G + P + LQK  
 Sbjct: 549 -----SENNEGHFGLAAENYTHFTSPIRRYPDLLVHRLI-REIGEGKTP---ANILQKWE 599

Query: 735 D 735  
 D  
 Sbjct: 600 D 600

>gi|21754656|dbj|BAC04542.1| unnamed protein product [Homo sapiens]  
 Length = 750

Score = 205 bits (521), Expect = 3e-51  
 Identities = 133/383 (34%), Positives = 197/383 (51%), Gaps = 32/383 (8%)

Query: 265 LFSPSDHRVPRIYVPLKDCP--QDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLG 322  
 L +P D+R+P+I + + QDF + RI W+ + G + LG  
 Sbjct: 366 LVTPWDYRIPKIRISTQQAETLQDFRV-----VVRIDSWESTSVYPNGHFVRVLG 415

Query: 323 QAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSL---PWTIPPDEVGKRRDLRKD-CIF 378  
 + G++E E IL E + FS + +P + PW + P+E KR+DLRK +F  
 Sbjct: 416 RIGDLEGEIATILVENSISVIPFSEAQMCEMPVNTPESPWKVSPEEEQKRKDLRKSHLVF 475

Query: 379 TIDPSTARDLDDALACRRLTDGTFEVGVIADVSFYFVPEGSSLDKVAAERATSVYLVQKV 438  
 +IDP D+DD L+ R L +G E+GVHIADV++FV S +D A RAT+ YL +  
 Sbjct: 476 SIDPKGCDVDDTLVRLNNGNLGLGVHIADVTHFVAPNSYIDIEARTRATTYYLADRR 535

Query: 439 VPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEG-KILEEWFGRTIIRSCTKLSYDHAQS 497  
 MLP +L +LCSL D+ S++W+L +I + W+GRTIIRS KL Y+ AQ  
 Sbjct: 536 YDMLPSVLSADLCSLLGGVDRYAVSIMWELDKASYEIKKVWYGRTIIRSAYKLFYEAQAE 595

Query: 498 MIENXXXXXXXXXXXXXXXXXHS----VEEVHQAVLNLHLSIAQLRRQRFVDGALRLDQLK 553  
 +++ S +EE+ A+ L IA+ +R +R GAL L+ ++  
 Sbjct: 596 LLDGNLSVVDDIPEFKDLGEKSQAKLEELVWAIGKLTDIARHVRAKRDGCGALELEGVE 655

Query: 554 LAFTLD-----HETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRH 608  
 + LD H+ Q ++E V E M+LAN VA KI+ +FP QALLR+H  
 Sbjct: 656 VCVQLDDKKNHDLIPKQPLEVHE-----TVAECMILANHWVAKKIWESFPHQALLRQH 709

Query: 609 PPPQTKMLSDLVEFCQMGLPMD 631  
 PPP + S+L E G +D  
 Sbjct: 710 PPPHQEFFSELRECAKAKGFFID 732

Score = 59.3 bits (142), Expect = 3e-07  
 Identities = 33/82 (40%), Positives = 51/82 (62%), Gaps = 8/82 (9%)

Query: 50 FETYSKEDVSEGLKRGTLIQGVLRLNPKKFH-EAFI-----PSPDGD--RDIFIDGVVA 101  
 + ++ E + G+K G IQG+L +N + EAF+ S D D DI I G+ A  
 Sbjct: 225 YPEHLPLEVLEAGIKSGRYIQGILNVNKHRAQIEAFVRLQGASSKSDSLVSDILIHGMKA 284

Query: 102 RNRALNGDLVVVKLLPEDQWKA 123  
 RNR+++GD+VVV+LLP+++WK  
 Sbjct: 285 RNRSIHGDDVVVVLELLPKNEWKG 306

>gi|23020108|gb|ZP\_00059814.1| hypothetical protein [Clostridium  
 thermocellum ATCC 27405]  
 Length = 757

Score = 203 bits (516), Expect = 1e-50  
 Identities = 153/510 (30%), Positives = 245/510 (48%), Gaps = 50/510 (9%)

Query: 232 KVVYILEKK---HSRAATGILKLLADKNSDLF-----KKYALFSPSDHRVP-RIYVPLK 281  
 +V+ + KK RA I+K++ N + K + P D R+ I++  
 Sbjct: 108 RVIRARINKKGIGDKRAEGEIIKIVKRANKTVVGTFFESSKYFGFVVPDDPRISGDIFI--- 164

Query: 282 DCPQDFMTRPKDFANTLFICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVD 341  
 P+D + K + + I+ W E A G++ + +G E + I+ Y +  
 Sbjct: 165 --PKDEINGAK--SGQKVVAEIVVWPEKRRNAEGRIIEIIGDKDEPGSDILSIKAYNLR 220

Query: 342 FSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGT 401  
 DF EV+ +S+ T+ D + RDLR + TID A+DLDDA++ RL +G  
 Sbjct: 221 -EDFPEEVIR-EAKSISQTVTDMIKGRRDLRLDTMTVIDGEDAKDLDDAVSIERLENGN 278

Query: 402 FEVGVHIADVSYFVPEGSSLDKVAERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLT 461  
 + +GVHIADVSY+V EGS LDK A +R TSVYLV +V+PM P+ L +CSLNP D+L  
 Sbjct: 279 YRLGVHIADVSYVKEGSPLDKEALKRGTSVYLVDRVIPMPFKELSNIGCSLNPKVDRLA 338

Query: 462 FSVIWKLTPEGKILEEWFGRRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVE 521  
 F+V+ ++ G++++ ++I +++Y ++E H+++  
 Sbjct: 339 FTVMEIDKSGRVVDHEIFESVINVNERMTYTDVYKILEENDEGLIERYKYLCDTFHTMK 398

Query: 522 EVHQAVLNLHLSIAQLRRQRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVE 581  
 E +A LR++R GA+ + + LD E G+P YE +N ++E  
 Sbjct: 399 E-----LALILRKKRMDRGAI DFNFEAKIVLD-EKGVPIEVKRYEMTIANNIE 447

Query: 582 EFMLLANMAVAHKIFRTFPEQALLRRHPPQTKMLSDLVEFCQMGLPMDVSSAGALNKS 641  
 EFML+ N VA F T + R H P + EF +G + +NK  
 Sbjct: 448 EFMLVCNETVAEHFFWT-NTPFVYRIHEDPDPDKIEAFSEFVHNLGYTLK-----GINKI 501

Query: 642 LTKTFGD--DKYSLARKE-VLTNMYSRPMQMALY--FCSGMLQDQEQFRHYALNVPLYTH 696  
 K D +K ++E +++ + R +Q A Y SG H+ L Y H  
 Sbjct: 502 HPKALQDVLEKARGTKEETIISTVMLRSLQKARYSHINSG-----HFGLAAKYYCH 552

Query: 697 FTSPIRRFAADVIVHRLLAALGYSEQPDVE 726

FTSPIRR+ D+I+HR++ L + P+ E  
Sbjct: 553 FTSPIRRYPDLIIHRIMKEYLKGTVPNPERE 582

>gi|16801605|ref|NP\_471873.1| similar to exoribonuclease RNase-R [Listeria innocua]  
gi|25298866|pir|AB1750 exoribonuclease RNase-R homolog lin2543 [imported]  
- Listeria

innocua (strain Clip11262)  
gi|16415065|emb|CAC97770.1| similar to exoribonuclease RNase-R [Listeria innocua]

Length = 793

Score = 201 bits (512), Expect = 3e-50

Identities = 138/430 (32%), Positives = 219/430 (50%), Gaps = 39/430 (9%)

Query: 313 ALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDL 372  
A G + +G + + I+ ++G+ + F EV+E + ++ P + ++G RRDL

Sbjct: 195 ARGVVKSIIGHRNDPGVDILSIIHKHGISIA-FPEEVMEQVSKA-PDVVDDSDIGNRRDL 252

Query: 373 RKDCIFTIDPSTARDLDDALACRRLTDGTFEYGVHIAADVSYFVPEGSSLDKVAERATSV 432  
R I TID + A+DLDDA+ ++L +G +++GVHIAADV+++V EGS LDK A +R TSV

Sbjct: 253 RDQMIITIDGADAKDLDDAVTVKQLPNGNWKLGVHIAADVTHYVTEGSPLDKEAQDRGTSV 312

Query: 433 YLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRITIRSECTKLSY 492  
YLV +V+PMLP L +CSLNP D+ T S ++ EG ++ +II++ +++Y

Sbjct: 313 YLVDRVIPMLPHKLSNGICSLNPQVDRFTMSCEMEIDQEGHVVNHEIFESIIKTERMTY 372

Query: 493 DHAQSMIENXXXXXXXXXXXXXXXXXSVVEEVHQAVALNLHSIAKQLRRQRFVDGALRLDQL 552  
++ +++ +A+ LRR+R GA+ D

Sbjct: 373 TDVNDILVEKDEALREKYAPIVPMLEAMQH-----LAEILRRKREKRGALDFD-F 421

Query: 553 KLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPQ 612  
K A + E G P+ + E L+EEFML AN VA F + R H P+

Sbjct: 422 KEARVVVDEEGHPEEVVMRERSAGEHLIEEFMLAANETVAEH-FHWMVDPFIYRIHEDPK 480

Query: 613 TKMLSDLVEFCDQMGLPMDVSSAGALNKSILTKTFGDDKYSLARKEVLNMYSRPMQMALY 672  
L+ EF GL + K +D + A ++VL + +P +M +

Sbjct: 481 EDKLARFFEFITNFGL-----IVKGTANDIHPAALQQVLEEYKGPKEEMVV- 526

Query: 673 FCSGMLQDQEQFR-----HYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDV 725  
+ ML+ +Q + H+ L+ YTHFTSPIRR+ D+IVHRL+ Y DV

Sbjct: 527 -STVMLRSMQQAKYDTSAGHFGSLTDFYTHFTSPIRRYPDLIVHRLIRE---YLINGDV 582

Query: 726 EPDTLQKQAD 735  
P+TL+K+A+

Sbjct: 583 RPETLEKRAE 592

>gi|16804487|ref|NP\_465972.1| similar to exoribonuclease RNase-R [Listeria monocytogenes EGD-e]  
gi|25298867|pir|AI1380 exoribonuclease RNase-R homolog lmo2449 [imported]  
- Listeria

monocytogenes (strain EGD-e)  
gi|16411937|emb|CAD00527.1| similar to exoribonuclease RNase-R [Listeria monocytogenes]

Length = 793

Score = 200 bits (509), Expect = 7e-50

Identities = 138/430 (32%), Positives = 218/430 (50%), Gaps = 39/430 (9%)

Query: 313 ALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDL 372  
A G + +G + + I+ ++G+ F EV+E + ++ P + ++G RRDL

Sbjct: 195 ARGVVKSIIGHRNDPGVDILSIIHKHGISIG-FPEEVMEQVSKA-PDLVDDSDIGNRRDL 252

Query: 373 RKDCIFTIDPSTARDLDDALACRRLTDGTFEYGVHIAADVSYFVPEGSSLDKVAERATSV 432  
R I TID + A+DLDDA+ ++L +G +++GVHIAADV+++V EGS LD A ER TSV

Sbjct: 253 RDQMIITIDGADAKDLDDAVTVKQLPNCNWKLGVHIADVTHYVTEGSPLDIEAQERGTSV 312

Query: 433 YLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRRTIIRSCTKLSY 492  
 YLV +V+PMLP L +CSLNP D+ T S ++ EG ++ +II++ +++Y

Sbjct: 313 YLVDRVIPMLPHKLSNGICSLNPQVDRFTMSCEMEIDQEGHVVNHEIFESI IKTERMTY 372

Query: 493 DHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRRQRFVDGALRLDQL 552  
 ++ ++ ++A+ LRR+R GA+ D

Sbjct: 373 TDVNDILVEKDEALREKYAPIVPMLEAMQ-----NLAEILRRKREKRG AIDFD-F 421

Query: 553 KLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPQ 612  
 K A + E G P+ + E L+EEFML AN VA F + R H P+

Sbjct: 422 KEARVVVDEGDHPEAVVMRERSAGEHLIEEFMLAANETVAEH-FHWM DVPFIYRIHEDPK 480

Query: 613 TKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVL TNMYSRPMQMALY 672  
 L+ EF GL + K +D + A ++VL + +P +M +

Sbjct: 481 EDKLARFFEFITNFGL-----IVKGTANDIHPAALQQVLEE VKGKPEEMVV- 526

Query: 673 FCSGMLQDQEQFR-----HYALNVPLYTHFTSPIRRFADVIVHRLLAALGYSEQPDV 725  
 + ML+ +Q + H+ L+ YTHFTSPIRR+ D+IVHRL+ Y DV

Sbjct: 527 -STVMLRSMQQAKYDTVSAGHFG LSTDFYTHFTSPIRRYPDLIVHRLIRE---YLINGDV 582

Query: 726 EPDTLQKQAD 735  
 P+TL+K+A+

Sbjct: 583 RPETLEKRAE 592

>gi|21397569|ref|NP\_653554.1| RNB, RNB-like protein [Bacillus anthracis A2012]

Length = 808

Score = 197 bits (501), Expect = 7e-49  
 Identities = 133/414 (32%), Positives = 214/414 (51%), Gaps = 22/414 (5%)

Query: 300 ICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPW 359  
 + +I + E+ A G++ + LG + + ++ ++ + + F EV+E S+P

Sbjct: 185 VVKITSYPENRLSAEGEVIQILGHKNDPGVDILSVIHKHHLPLA-FPEEVME-HANSVPE 242

Query: 360 TIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFE VGVHIADVSYFVPEGS 419  
 TI +++ RRDLR I TID + A+DLDDA+ +L +G +++GVHIADVSV+V EGS

Sbjct: 243 TISEEDLKDRRDLRDQMIVTIDGADAKDLDDAVTVTKLENGNYKLGVHIADVSHYVQEGS 302

Query: 420 SLDKVA AERATSVYLVQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWF 479  
 +D AAERATSVYLV +V+PM+P L +CSLNP D+LT S ++ G +++

Sbjct: 303 PIDVEAAERATSVYLVDRVIPMIPHRLSNGICSLNPKVDRLTLSCEMEINN LGDVVKHEI 362

Query: 480 GRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRR 539  
 +++I++ +++Y +S++E+ E + + +A+ LR

Sbjct: 363 FQSVIKTTERMTYADVRSILEDEDEELMKRY-----EPLVPMFKEMGQLAQILRE 412

Query: 540 QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTF 599  
 +R GA+ D K A L E G P + + S KL+EEFML+AN VA F

Sbjct: 413 KRMRRGAIDFD-FKEAKVLVDEEGKPTDVVMRDRSVSEKLIEEFMLVANETVAEH-FHWM 470

Query: 600 PEQALLRRHPPPTKMLSDLVEFCDQMGLPMDVSSAGALNKS LTKTFGDDKYSLARKEVL 659  
 + R H P+ L EF G + + ++L + + + V+

Sbjct: 471 NVPFMYRVHEDPKEDKLERFFEFVTNFGYAVKGRANEVHPRALQQIL-EMVQGPPEEVVI 529

Query: 660 TNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRL 713  
 + + R M+ A Y D + H+ L+ YTHFTSPIRR+ D IVHRL+

Sbjct: 530 STVMLRSMKQARY-----DADSLGHFGLSTEFYTHFTSPIRRYPDTIVHRLI 576

>gi|16080414|ref|NP\_391241.1| similar to hypothetical proteins [Bacillus subtilis]

gi|7674332|sp|O32231|RNR\_BACSU Ribonuclease R (RNase R) (VacB protein homolog)

gi|7443068|pir||G70027 conserved hypothetical protein yvaJ - Bacillus subtilis  
gi|2635874|emb|CAB15366.1| similar to hypothetical proteins [Bacillus subtilis]

Length = 779

Score = 195 bits (495), Expect = 3e-48  
Identities = 131/418 (31%), Positives = 213/418 (50%), Gaps = 22/418 (5%)

Query: 300 ICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPW 359  
+ ++ + E A G++ LG + + ++ ++G+ +F ++ +E S P  
Sbjct: 181 VVKLTSYPEGRMNAEGEVETILGHKNDPGIDILSVIHKHGLP-GEFPADAME-QASSTPD 238

Query: 360 TIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGS 419  
TI ++ RRDLR I TID + A+DLDDA+ +L DG++++GVHIADVS++V E S  
Sbjct: 239 TIDEKDLKDRRLDRDQVIVITIDGADAKDLDDAVTVTKLDDGSYKLGVHIADVSHYVTENS 298

Query: 420 SLDKVAERATSVYLVQKVPMPLRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWF 479  
+DK A ER TSVYLV +V+PM+P L +CSLNP D+LT S + +G++ E  
Sbjct: 299 PIDKEALERGTSVYLVDRVIPMIPHRLSNGICSLNPKVDRLTLSCMTINSQGVTEHEI 358

Query: 480 GRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRR 539  
+++I++ +++Y ++ + E + ++ +A+ LR  
Sbjct: 359 FQSVIKTTERMTYSVDNKKILVD-----DDEELKQKYEPLVPMFKDMERLAQILRD 408

Query: 540 QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYERYDSNKLVEEFMLLANMAVAHKIFRTF 599  
+R GA+ D K A L + G + I E + KL+EEFML+AN VA F  
Sbjct: 409 KRMDRGAVDFD-FKEAKVLVDDEGAVKDVVIRERSVAEKLIEEFMLVANETVAEH-FHWM 466

Query: 600 PEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSSAGALNKSILTKTFGDDKYSLARKEVL 659  
+ R H P + L +EF G + +AG ++ ++ D + V+  
Sbjct: 467 NVPFIYRIHEEPNAEKLQKFLEFVTTFGYVVK-GTAGNIHPRALQSILDAVRDRPEETVI 525

Query: 660 TNMYSRPMQMALYFCSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLLAAL 717  
+ + R M+ A Y D + H+ L+ YTHFTSPIRR+ D+IVHRL+ L  
Sbjct: 526 STVMLRSMKQAKY-----DPQSLGHFGLSTEFYTHFTSPIRRYPDLIVHRLIRTYL 576

>gi|15894003|ref|NP\_347352.1| FUSION ribonuclease and ribosomal protein S1 domain [Clostridium

acetobutylicum]

gi|25298861|pir||A96988 FUSION ribonuclease and ribosomal protein S1 domain [imported] -

Clostridium acetobutylicum

gi|15023595|gb|AAK78692.1|AE007586\_9 FUSION ribonuclease and ribosomal protein S1 domain [Clostridium

acetobutylicum]

Length = 730

Score = 190 bits (483), Expect = 7e-47  
Identities = 128/420 (30%), Positives = 213/420 (50%), Gaps = 35/420 (8%)

Query: 300 ICRIIDWKEDCNFALGQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPW 359  
+ I W + G++ + +G GE + I+ ++ + E +E + +P  
Sbjct: 177 VAEITVWPKRRNPEGKIVEIIGSKGEGVDILTIIKKH--KLPEKFPEKVERFAEGIPN 234

Query: 360 TIPPDEVGKRRDLRKDCIFTIDPSTARDLDDALACRRLTDGTFEVGVHIADVSYFVPEGS 419  
IP E +RRD+R + TID A+DLDDA++ +L++G F++GVHIADVS +V E +  
Sbjct: 235 EIPSEYKRRRDIRDKMVTIDGEDAKDLDDAVSIEKLSNGNFKLGVHIADVSNYVREDN 294

Query: 420 SLDKVAERATSVYLVQKVPMPLRLLCEELCSLNPMTDKLTFSVIWKLTPGKILEEWF 479  
LDK A +RATSVYL+ +V+PMLP+ L +CSLNP D+L S ++ P GK+++  
Sbjct: 295 PLDKALKRATSVYLIDRVIPMLPKKLSNGICSLNPRQDRLAMSCFMEIDPTGKVIQHEI 354

Query: 480 GRTIIRSCTKLSYDHAQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQAVLNLHSIAKQLRR 539  
+II++ +++Y ++ + + E ++ N+ +A L +

Sbjct: 355 FESIIKTNERMTYTDVTKILRD-----HDEETIKAFEYLYDDFKNMEELASILNK 404

Query: 540 QRFVDGALRLDQLKLAFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVA-HKIFRT 598  
 +R + GA+ D + TL+ E G P YE +N+++EEFML+ N +A H +

Sbjct: 405 KRLLRGAIDFDFEESKITLN-ELGKPEVEKPYERAVANRIIEEFMLVCNETIAEHFYWAN 463

Query: 599 FPEQALLRRHPPPQTKMLSDLVEFCDQMGLPMDVSS---AGALNKS�TKTFGDDKYSLAR 655  
 P + R H P ++ L EF +G + S L + K G +

Sbjct: 464 IP--FVYRVHEEPDSEKLERFNEFIHNLGYAVRWGSEVHPKQLQDVIEKIKGKKE----- 516

Query: 656 KEVLTNMYSRPMQMALYF--CSGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRL 713  
 + V++ + R ++ A Y CSG H+ L Y HFTSPIRR+ D+I+HR++

Sbjct: 517 ETVVSTLLLRSLKQARYSPEC SG-----HFGLAARYYCHFTSPIRRYPDLIIHRIM 567

>gi|27467483|ref|NP\_764120.1| ribonuclease R [Staphylococcus epidermidis  
 ATCC 12228]  
 gi|27315026|gb|AAO04162.1|AE016745\_261 ribonuclease R [Staphylococcus  
 epidermidis ATCC 12228]  
 Length = 792

Score = 190 bits (483), Expect = 8e-47  
 Identities = 132/430 (30%), Positives = 215/430 (50%), Gaps = 26/430 (6%)

Query: 315 GQLAKSLGQAGEIEPETEGILTEYGVDFSDFSSEVLECLPQSLPWTIPPDEVGKRRDLRK 374  
 G ++ LG + + I+ ++G++ +F +VL+ + +P I P E+ RRDLR

Sbjct: 199 GHVSAILGHKNDPGVDILSIIYQHGI EI-EFPDDVLQ-EAEEVPDVIEPSEIEGRDDL RD 256

Query: 375 DCIFTIDPSTARDLDDALACRLTDGTFEYGVHIAVSVYFVPEGSSLDKVAERATSVYL 434  
 + TID + A+DLDDA+A ++L +G E+ V IADVSY+V EGS+LDK A +RATSVYL

Sbjct: 257 ELTITIDGADAKDLDDAIAVKKLKNGNTELTVSIADVSYVKEGSALDKEAYDRATSVYL 316

Query: 435 VQKVVPMLPRLLCEELCSLNPMTDKLTFSVIWKLTPEGKILEEWFGRITIRCTKLSYDH 494  
 V +V+PM+P L +CSLNP D+LT S ++ G++++ ++I S +++YD

Sbjct: 317 VDRVIPMIPHRLSNGICSLNPEEDRLTLSCRMEINERGEVVKHEIFDSVIHSNYRMTYDA 376

Query: 495 AQSMIENXXXXXXXXXXXXXXXXXHSVEEVHQA VLNHLHSIAKQLRRQRFVDGALRLDQLKL 554  
 +I + ++ ++ +L R R G + D +

Sbjct: 377 VNKIITDQDSEIRSQYKDLTPMLDLAQD-----LSNRLIRMKRKRGEIDFD-INE 425

Query: 555 AFTLDHETGLPQGCHIYEYRDSNKLVEEFMLLANMAVAHKIFRTFPEQALLRRHPPPQTK 614  
 A L ++ G+P + E + +L+E FML AN VA F + R H P++

Sbjct: 426 AKVLVNDEGIPTVLMRERGERGERLIESFMLAANETVAEH-FNKLEVPIYRVHEQPKSD 484

Query: 615 MLSDLVEFCDQMGLPMDVSSAGALNKS�TKTFGDDKYSLARKEVLTNMYSRPMQMALYFC 674  
 L +F G+ M + ++ + + ++ + V++ M R MQ A Y

Sbjct: 485 RLRQFFDFITNFGI-MIKGTGEDIHPTTLQNIQEVEGRPEQM VISTMMLRSMQQAHY-- 541

Query: 675 SGMLQDQEQFRHYALNVPLYTHFTSPIRRFADVIVHRLAALGYSEQPDVE---PDTL 730  
 D H+ L+ YTHFTSPIRR+ D+ VHRL+ L + E +TL

Sbjct: 542 -----DDVNLGHFGLSAEYTHFTSPIRRYPDLTVHRLIRKYLIENSMDKKEIRHWEETL 596

Query: 731 QKQADHCNDR 740  
 + A+H + R

Sbjct: 597 PELAEHTSQR 606

Database: All non-redundant GenBank CDS  
 translations+PDB+SwissProt+PIR+PRF  
 Posted date: Jan 29, 2003 9:26 AM  
 Number of letters in database: 423,161,544  
 Number of sequences in database: 1,321,324

Lambda	K	H
0.319	0.136	0.399

Gapped



Lambda      K      H  
0.267      0.0410      0.140

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Hits to DB: 681,347,984  
Number of Sequences: 1321324  
Number of extensions: 28649337  
Number of successful extensions: 62317  
Number of sequences better than 10.0: 242  
Number of HSP's better than 10.0 without gapping: 232  
Number of HSP's successfully gapped in prelim test: 10  
Number of HSP's that attempted gapping in prelim test: 61354  
Number of HSP's gapped (non-prelim): 402  
length of query: 870  
length of database: 423,161,544  
effective HSP length: 132  
effective length of query: 738  
effective length of database: 248,746,776  
effective search space: 183575120688  
effective search space used: 183575120688  
T: 11  
A: 40  
X1: 16 ( 7.4 bits)  
X2: 38 (14.6 bits)  
X3: 64 (24.7 bits)  
S1: 41 (21.7 bits)  
S2: 77 (34.3 bits)